

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 11:52:56 ; Search time 219.652 Seconds
(without alignments)
646.813 Million cell updates/sec

Title: US-10-041-030-8
Perfect score: 24
Sequence: 1 ccagtagtttagcttggctt 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	6	ABQ78314
2	24	100.0	259	8	Abq78314 Probe N63
3	24	100.0	554	6	Abt18999 Group III
4	24	100.0	864	4	Abt10524 Human bre
5	24	100.0	3614	4	Aah34231 Human col
6	24	100.0	3615	4	Aal04355 Human rep
7	24	100.0	3752	4	Aal04354 Human rep
8	24	100.0	5579	8	Aal04353 Human rep
9	19.2	80.0	2202	9	Acc42349 Human MAP
10	19.2	80.0	2202	12	Abd70333 Thyroid t
11	19.2	80.0	3293	4	Adj37112 Human mal
12	19.2	80.0	3293	2	Aat05810 Human thy
13	18.4	76.7	473	13	Aas11829 Human TTF
14	18.2	75.8	621	12	Adq56478 Novel can
15	18.2	75.8	110000	12	Adk16049 Nantoarcha
16	18.2	75.8	143239	12	Adk16049 Nantoarcha
17	17.8	74.2	452	3	Adq17729 Human sof
18	17.6	73.3	474	6	Aaa43756 Human sec
19	17.6	73.3	549	6	Abt03344 Ovary cel
20	17.6	73.3	262090	12	Abk95242 Human pro
					Adq59207 MSI-H car

C	21	17.4	72.5	504	9	ACH38322	Ach38322 Human end
C	22	17.4	72.5	2366	8	ABX10385	Abx10385 DNA encod
C	23	17.4	72.5	2366	13	ADR25645	Adr25645 Breast ca
	24	17.2	71.7	1512	6	ABL42100	AbL42100 Nucleotid
	25	17.2	71.7	15275	4	AAS35975	Aas35975 Human car
	26	17.2	71.7	15275	10	ADE46669	Ade46669 Human car
	27	17.2	71.7	15275	13	ADJ08087	Adj08087 Human car
	28	17.2	71.7	106344	10	ADJ79961	Adj79961 Full leng
	29	17	70.8	101786	3	Aaf22293	Aaf22293 BAC conta
	30	16.8	70.0	514	10	ADC26745	Adc26745 Human lip
C	31	16.8	70.0	564	6	ABQ55470	Abq55470 Human ova
C	32	16.8	70.0	790	2	AAV20469	Aav20469 Human c-r
	33	16.8	70.0	807	6	ABZ42929	Abz42929 Human GPC
	34	16.8	70.0	927	4	AAH31701	Aah31701 Human olf
	35	16.8	70.0	927	12	ADG76823	Adg76823 Human olf
	36	16.8	70.0	958	4	AAH31707	Aah31707 Human olf
	37	16.8	70.0	966	6	ABT04196	Abt04196 Human G-p
	38	16.8	70.0	966	12	ADH30931	Adh30931 Human G-p
	39	16.8	70.0	978	5	AA842325	Aas42325 Human GPC
	40	16.8	70.0	978	6	ABZ43023	Abz43023 Human GPC
	41	16.8	70.0	978	6	ABK68498	Abk68498 Human DNA
	42	16.8	70.0	978	6	ABK37611	Abk37611 DNA encod
	43	16.8	70.0	978	12	ADG83373	Adg83373 Human Olf
	44	16.8	70.0	1014	8	ABZ58237	Abz58237 Human G-p
	45	16.8	70.0	1330	10	ADC85636	Adc85636 Human GPC

ALIGNMENTS

RESULT 1
ABQ78314
ID ABQ78314 standard; DNA; 24 BP.
XX
AC ABQ78314;
XX

DT 05-NOV-2002 (first entry)

DE Probe N63226QR to detect Pellino 2 gene in cancer cells.

XX Pellino 2; cancer; Pellino 1; cancer treatment; epithelial cancer;
KW gastrointestinal tract cancer; probe; ss.
XX Homo sapiens.

PN WO200259611-A2.

PD 01-AUG-2002.

PF 28-DEC-2001; 2001WO-US051368.

PR 02-JAN-2001; 2001US-0259502P.

XX (TUL) TULARIK INC.

XX Powers S, Mu D, Xiang P, Peng Y;

XX WPI; 2002-619185/66.

XX Detecting cancer cells in mammalian sample, useful for identifying
XX inhibitors for treating cancer e.g. epithelial cancer, comprises
XX detecting an overexpression of, or increase in copy number of genes
XX encoding, Pellino 1 and Pellino 2.

XX Example 2; Page 55; 69pp; English.

XX Probes ABQ78313-15 were used to detect human Pellino 2 gene in cancer
XX cells. The specification describes a method for detecting cancer cells in
XX biological sample from a mammal. The method comprises detecting an
XX overexpression of, or increase in copy number of genes encoding,
XX polypeptides Pellino 1 or Pellino 2. The method is useful in detecting
XX cancer or propensity to develop cancer, monitoring the efficacy of cancer
XX treatment, identifying inhibitors of Pellino 1 and 2, inhibiting the

CC expression and/or activity of Pellino 1 and 2 in cancer cells, and
 CC treating cancer or inhibiting proliferation of cancer. The cancer can be
 CC epithelial cancer, such as lung, colon, ovarian, breast, prostate,
 CC kidney, stomach, bladder, or any cancer of the gastrointestinal tract
 XX
 SQ Sequence 24 BP; 3 A; 5 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0;

Qy 1 CCAGTAGTTAGCCTTTGGCTT 24
 |||||
 Db 1 CCAGTAGTTAGCCTTTGGCTT 24

RESULT 2
 ABZ18999/c
 ID ABZ18999 standard; cDNA; 259 BP.

XX ABZ18999;
 XX
 XX
 DT 23-JAN-2003 (first entry)
 XX
 XX
 DE Group III cDNA cancer related clone SEQ ID NO:1425.

XX Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;
 KW immune response; virology; immunology; microbiology; molecular biology;
 KW recombinant DNA technology; gene; ss.

XX Homo sapiens.

XX WO200278516-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US010421.

XX 30-MAR-2001; 2001US-0280255P.

PR 28-AUG-2001; 2001US-0315563P.

PR 09-JAN-2002; 2002US-0347313P.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang S, Bangur CS, Gaiger A;

XX WPI; 2003-058387/05.

XX New immunogenic polynucleotides or polypeptides useful for diagnosing,
 PT preventing and treating cancer expressing CT or CP mRNA antigens, and in
 PT virology, immunology, microbiology, molecular biology and recombinant DNA
 PT techniques.

XX Claim 1; SEQ ID NO 1425; 207pp; English.

XX ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and
 CC ABP5446 to ABP54472 represent protein (II) sequences, from the present
 CC invention. (I) and (II) have cytostatic activity and can be used in gene
 CC therapy and vaccines. (I), (II), antibodies and compositions from the
 CC present invention are useful for diagnosing, preventing and treating
 CC cancer, which expresses CT or CP mRNA antigens. They are useful for
 CC stimulating immune response. They can also be useful in virology,
 CC immunology, microbiology, molecular biology and recombinant DNA
 CC techniques. N.B. The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 259 BP; 89 A; 50 C; 59 G; 61 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 8; Length 259;
 Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0;

Qy 1 CCAGTAGTTAGCCTTTGGCTT 24
 |||||
 Db 79 CCAGTAGTTAGCCTTTGGCTT 56

RESULT 3

ABT10524/c
 ID ABT10524 standard; cDNA; 554 BP.

XX AC ABT10524;
 XX
 DT 04-DEC-2002 (first entry)
 XX

XX Human breast cancer associated coding sequence SEQ ID NO: 658.

DE Human; breast specific gene; breast cancer; differential expression;
 KW cytosolic; gene therapy; gene; ss.

XX Homo sapiens.

XX WO200259271-A2.

XX 01-AUG-2002.

XX 25-JAN-2002; 2002WO-US002176.

XX 25-JAN-2001; 2001US-0263757P.

PR 25-APR-2001; 2001US-0286090P.

PR 23-MAY-2001; 2001US-0292517P.

XX (GENE-) GENE LOGIC INC.

XX Orr MS, Nation M, Diggans JC, Zeng W;

XX WPI; 2002-674803/72.

XX Diagnosing breast cancer in a patient comprises detecting the level of
 PT gene expression in cell or tissue samples, where a differential gene
 PT expression is indicative of breast cancer.

XX Claim 1; SEQ ID NO 658; 260pp + Sequence Listing; English.

XX The present invention relates to methods of diagnosing breast cancer in a
 CC patient, which comprise detecting the level of expression in a tissue
 CC sample of two or more genes selected from those shown in ABT09867-
 CC ABT1112, where a differential expression of the genes indicates breast
 CC cancer. The methods are useful in diagnosing, treating, detecting the
 CC progression, and in monitoring treatment of breast cancer in patients.
 CC The methods are also useful as a screening tool for agents that modulate
 CC the onset or progression of breast cancer. The breast cancer genes may be
 CC used as diagnostic markers for the prediction or identification of the
 CC malignant state of breast tissue, for confirming the type and progression
 CC of cancer, and for drug screening and assays. The present sequence is a
 CC coding sequence of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 554 BP; 196 A; 88 C; 92 G; 178 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 6; Length 554;
 Best Local Similarity 100.0%; Pred. No. 0.27; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0;

Qy 1 CCAGTAGTTAGCCTTTGGCTT 24
 |||||
 Db 519 CCAGTAGTTAGCCTTTGGCTT 496

RESULT 4

AAH34231
 ID AAH34231 standard; cDNA; 864 BP.

XX

AC AAH34231;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1313.
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; ss.
XX
XX Homo sapiens.
OS
XX
XX W0200122920-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 28-SEP-2000; 2000WO-US026524.
PF
XX
XX 29-SEP-1999; 99US-0157137P.
PR
XX 03-NOV-1999; 99US-0163280P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Ruben SM, Baraah SC, Birse CE, Rosen CA;
PI
XX WPI; 2001-235357/24.
XX P-PSDB; AAG74826.
DR
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.
PT
XX
XX Claim 1; Page 3049; 9803pp; English.
PS
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patient's own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37195 to AAH37204 and AAG77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 866 to 882 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
SQ Sequence 864 BP; 247 A; 143 C; 157 G; 314 T; 0 U; 3 Other;

Query Match 100.0%; Score 24; DB 4; Length 864;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGGCTT 24
Db 260 CCAGTAGTTAGCCTTTGGCTT 283

RESULT 5
AAL04355
ID AAL04355 standard; DNA; 3614 BP.
XX
XX AAL04355;
XX
XX 21-NOV-2001 (first entry)
DT
DE Human reproductive system related antigen DNA SEQ ID NO: 7043.
XX
XX Human; reproductive system related antigen; reproductive system disorder;
KW

KW cancer; gene therapy; ds.
XX
XX Homo sapiens.
OS
XX W0200155320-A2.
PN
XX
XX 02-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US001339.
PF
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226682P.
PR 22-AUG-2000; 2000US-0226688P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.

PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0241826P.
PR 08-NOV-2000; 2000US-0246471P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250331P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-02559678P.

XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465570/50.
XX Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
XX PT
XX PS
XX Disclosure; SEQ ID NO 7043; 1297pp + Sequence Listing; English.
XX The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders including cancer. The present sequence is a genomic sequence encoding a protein of the invention
XX CC
XX SQ
XX Sequence 3614 BP; 1063 A; 621 C; 657 G; 1273 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 24; DB 4; Length 3614;
XX Best Local Similarity 100.0%; Pred. No. 0.34; Length 3614;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CCAGTAGTTAGCCTTTGTGGCTT 24
Db 3012 CCAGTAGTTAGCCTTTGTGGCTT 3035
RESULT 6
AAL04354
ID AAL04354 standard; DNA; 3615 BP.
XX AC AAL04354;
XX DT 21-NOV-2001 (first entry)
XX DE Human reproductive system related antigen DNA SEQ ID NO: 7042.
XX KW Human; reproductive system related antigen; reproductive system disorder;
XX KW cancer; gene therapy; ds.
XX OS Homo sapiens.
XX PN WO200155320-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US001339.
XX PR 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 24-FEB-2000; 2000US-0184664P.
XX PR 02-MAR-2000; 2000US-0186350P.
XX PR 16-MAR-2000; 2000US-0189874P.
XX PR 17-MAR-2000; 2000US-0190076P.
XX PR 18-APR-2000; 2000US-0198123P.
XX PR 19-MAY-2000; 2000US-0205515P.
XX PR 07-JUN-2000; 2000US-0209467P.
XX PR 28-JUN-2000; 2000US-0214866P.
XX PR 30-JUN-2000; 2000US-0215135P.
XX PR 07-JUL-2000; 2000US-0216647P.
XX PR 07-JUL-2000; 2000US-0216880P.
XX PR 11-JUL-2000; 2000US-0217487P.
XX PR 11-JUL-2000; 2000US-0217496P.
XX PR 14-JUL-2000; 2000US-0218290P.
XX PR 26-JUL-2000; 2000US-0220963P.
XX PR 26-JUL-2000; 2000US-0220964P.
XX PR 14-AUG-2000; 2000US-0224518P.
XX PR 14-AUG-2000; 2000US-0224519P.
XX PR 14-AUG-2000; 2000US-0225213P.
XX PR 14-AUG-2000; 2000US-0225214P.
XX PR 14-AUG-2000; 2000US-0225266P.

Thu Jul 21 09:13:22 2005

us-10-041-030-8.rng

AC AAL04353;
XX 21-NOV-2001 (first entry)
DT Human reproductive system related antigen DNA SEQ ID NO: 7041.
TX DE Human; reproductive system related antigen; reproductive system disorder;
XX KW cancer; gene therapy; ds.
XX OS Homo sapiens.
XX WO20015320-A2.
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US001339.
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0215135P.
PR 30-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0226279P.
PR 18-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232337P.
PR 14-SEP-2000; 2000US-0232338P.
PR 14-SEP-2000; 2000US-0232339P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0255147P.

```

PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254037P.
PR 05-JAN-2001; 2001US-02559678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465570/50.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen is
XX used in preventing, treating or ameliorating a medical condition.
XX
XX Disclosure; SEQ ID NO 7041; 1297pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
XX number of human reproductive system related antigens. These can be used
XX in the prevention and treatment of reproductive system disorders,
XX including cancer. The present sequence is a genomic sequence encoding a
XX protein of the invention
XX
XX Sequence 3752 BP; 1101 A; 648 C; 671 G; 1332 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 24; DB 4; Length 3752;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGGCTT 24
DB 3013 CCAGTAGTTAGCCTTTGGCTT 3036

RESULT 8
ACC42349
ID ACC42349 standard; cDNA; 5579 BP.
XX
XX ACC42349;
XX
XX 22-MAY-2003 (first entry)
XX
XX Human MAP kinase cascade activator #59 cDNA.
XX
XX Human; Elki phosphorylation; Elki phosphorylation kinase; virucide;
XX antiinflammatory; immunomodulator; cytostatic; antiallergic; anti-HIV;
XX antirheumatic; antiarthritic; antidiabetic; antiasthmatic; gene therapy;
XX inflammation; autoimmune disease; viral disease; cancer; diabetes;
XX rheumatoid arthritis; asthma; allergic rhinitis; AIDS; viral hepatitis;
XX Iga nephritis; gene; ss.
XX
XX Homo sapiens.
XX
XX WO2003008589-A1.
XX
XX 30-JAN-2003.
XX
XX 15-JUL-2002; 2002WO-JP007174.
XX
XX 18-JUL-2001; 2001JP-00218204.
XX 31-AUG-2001; 2001JP-00263450.
XX 21-JAN-2002; 2002JP-00012176.
XX
XX (ASAH ) ASahi KASEI KOGYO KK.
XX
XX Matsuzaki O, Matsuda A, Nagano Y, Suzuki N;
XX
XX WPI; 2003-229582/22.
XX P-PSDB; ABR41083.
XX
XX Elki phosphorylation-associated gene and its encoded protein with MAP

PT kinase cascade effect, applicable in diagnosis of and developing drugs
PT for e.g. inflammations, autoimmune diseases, viral diseases and cancer.
XX
XX Claim 4; Page 631-640; 762pp; Japanese.
XX
XX The invention relates to a novel purified protein having Elki
XX phosphorylation activity and/or an activity of activating Elki
XX phosphorylation kinase. A protein of the invention has antinflammatory,
XX immunomodulator, virucide, cytostatic, antiallergic, antirheumatic,
XX antiarthritic, antidiabetic, antiasthmatic, and anti-HIV activity. The
XX polynucleotides may have a use in gene therapy. The gene and its encoded
XX protein are applicable in diagnosis of and developing drugs for e.g.
XX inflammations, autoimmune diseases, viral diseases and cancer such as
XX rheumatoid arthritis, diabetes; asthma, allergic rhinitis, AIDS, viral
XX hepatitis and Iga nephritis. The present sequence is used in the
XX exemplification of the invention
XX
XX Sequence 5579 BP; 1535 A; 1111 C; 1214 G; 1719 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 24; DB 8; Length 5579;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGGCTT 24
DB 5062 CCAGTAGTTAGCCTTTGGCTT 5085

RESULT 9
ADB70333/c
ID ADB70333 standard; cDNA; 2202 BP.
XX
XX ADB70333;
XX
XX 04-DEC-2003 (first entry)
XX
XX Thyroid transcription factor 1 cDNA SEQ ID NO:25.
XX
XX cancer; malignant pleural mesothelioma; MP; lung adenocarcinoma;
XX squamous carcinoma; medulloblastoma; prostate cancer; breast cancer;
XX diffuse large B-cell lymphoma; follicular lymphoma; ovarian cancer;
XX human; gene; ss.
XX
XX Homo sapiens.
XX
XX WO2003021229-A2.
XX
XX 13-MAR-2003.
XX
XX 05-SEP-2002; 2002WO-US028203.
XX
XX 05-SEP-2001; 2001US-0317389P.
XX 30-AUG-2002; 2002US-00236031.
XX
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
XX
XX Gordon GJ, Jensen RV, Gullans SR, Bueno R;
XX
XX WPI; 2003-290233/28.
XX P-PSDB; ADB70370.
XX
XX Diagnosing cancer cells in tissue sample, or determining prognosis or
XX outcome of cancer patient, by calculating ratio of expression levels of
XX genes that are differentially expressed in cancer and non cancer tissues.
XX
XX Claim 67; Page 141-142; 396pp; English.
XX
XX The present invention describes a method (M1) for diagnosing the presence
XX of cancer cells or non-cancer cells in a tissue sample, or determining
XX the prognosis or outcome of a cancer patient. M1 involves providing a set
XX of genes that are differentially expressed in cancerous or non-cancerous
XX conditions, determining the expression levels of the set of genes and
XX calculating a ratio of the expression levels of the differentially

```

expressed genes. M1 is useful for diagnosing the presence of cancer cells or non-cancer cells in a tissue sample, where the cancer is malignant CC
 CC pleural mesothelioma (MPM), lung adenocarcinoma, squamous carcinoma, CC
 CC medulloblastoma, prostate cancer, breast cancer, diffuse large B-cell CC
 CC lymphoma, follicular lymphoma and ovarian cancer, and for determining CC
 CC prognosis or outcome of a cancer patient. The ratio of expression levels CC
 CC of differentially expressed genes is used as an indicator of cancer type, CC
 CC cancer class, and/or cancer prognosis, all of which are useful for CC
 CC determining a course of treatment of a patient. The present sequence CC
 CC encodes a human protein which is used in an example from the present CC
 CC invention.

Sequence 2202 BP; 503 A; 662 C; 643 G; 394 T; 0 U; 0 Other;
 Query Match 80.0%; Score 19.2; DB 9; Length 2202;
 Best Local Similarity 87.5%; Pred. No. 56;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCAGTAGTTTACGCTTTGGCTT 24
 ||||| ||||| ||||| ||||| |||||
 Db 1451 CCAGCAGTTTGGCTTTGGCTT 1428

RESULT 10
 ADJ37112/c
 ID ADJ37112 standard; cDNA; 2202 BP.

AC ADJ37112;
 XX
 XX 22-APR-2004 (first entry)

DE Human malignant pleural mesothelioma (MPM) cDNA #9.
 KW Human; malignant pleural mesothelioma; MPM; gene; ss; tumour;
 KW lung adenocarcinoma; squamous carcinoma; medulloblastoma;
 KW prostate cancer; breast cancer; diffuse large B-cell lymphoma;
 KW follicular lymphoma; ovarian cancer; cytostatic.

XX Homo sapiens.
 OS
 XX US2003219760-A1.
 PN
 XX
 XX 27-NOV-2003.
 PD
 XX
 XX 05-SEP-2002; 2002US-00236031.
 PF
 XX
 XX 05-SEP-2001; 2001US-0317389P.
 PR
 XX 30-AUG-2002; 2002US-0407431P.
 PR
 XX (SGHM) BRIGHAM & WOMENS HOSPITAL INC.

PA Gordon GJ, Jensen RV, Gullans SR, Bueno R;
 XX
 XX
 XX WPI; 2004-141744/14.
 DR
 XX P-PSDB; ADJ37113.

XX Diagnosing the presence of cancer or non-cancer cells in tissue sample,
 PT useful for diagnosing malignant pleural mesothelioma comprises
 PT determining ratio of expression level of a set of genes expressed in
 PT cancer tissues.

XX Claim 44; SEQ ID NO 25; 53pp; English.
 PS
 XX The invention relates to a method of diagnosing the presence of cancer
 CC cells or non-cancer cells in a tissue sample, determining prognosis or
 CC outcome of a cancer patient, selecting a course of treatment for a
 CC subject having or suspected of having malignant pleural mesothelioma
 CC (MPM) and evaluating treatment of MPM comprising determining the ratio of
 CC the expression level of a set of genes differentially expressed in a
 CC cancer tissue. The cancer is chosen from MPM, lung adenocarcinoma,
 CC squamous carcinoma, medulloblastoma, prostate cancer, breast cancer,
 CC diffuse large B-cell lymphoma, follicular lymphoma and ovarian cancer.
 CC The method is useful for diagnosing MPM in a subject suspected of having

CC MPM which involves obtaining a tissue sample suspected of being cancerous
 CC from a subject and determining the expression of nucleic acid markers or
 CC its expression products in the tissue sample. This sequence represents
 CC human MPM cDNA of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification but was obtained in
 CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 2202 BP; 503 A; 662 C; 643 G; 394 T; 0 U; 0 Other;
 Query Match 80.0%; Score 19.2; DB 12; Length 2202;
 Best Local Similarity 87.5%; Pred. No. 56;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCAGTAGTTTACGCTTTGGCTT 24
 ||||| ||||| ||||| ||||| |||||
 Db 1451 CCAGCAGTTTGGCTTTGGCTT 1428

RESULT 11
 AAT05810/c
 ID AAT05810 standard; DNA; 3293 BP.

AC AAT05810;
 XX
 XX 27-NOV-1996 (first entry)

DE Human thyroid transcription factor-1 gene.
 XX
 XX Thyroid transcription factor; TTF-1; human adenocarcinoma cell line;
 KW H441; rat; mouse; pulmonary adenocarcinoma; H820; small cell carcinoma;
 KW H345; tracheal-bronchial epithelial cell lines; respiratory epithelium;
 KW fecal lung; gestation; pro-SP-C; respiratory epithelial cell;
 KW nonciliated bronchiolar cell; immature lung; alveolar; Type II;
 KW epithelial cell; nonciliated; Type I; adult; ss.

OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH prim_transcript 143..3266
 FT /*tag= a
 FT exon 339..711
 FT /*tag= b
 FT intron 712..1674
 FT /*tag= c
 FT exon 1675..2417
 FT /*tag= d
 FT polyA_signal 3260..3266
 FT /*tag= e

XX WO9531729-A1.
 PN
 XX 23-NOV-1995.
 PD
 XX 17-MAY-1995; 95WO-US006244.
 PF
 XX 18-MAY-1994; 94US-00245356.
 PR
 XX (CHIL-) CHILDRENS HOSPITAL MEDICAL CENT.

PA Bohinski RJ, Whitsett JA;
 XX
 XX WPI; 1996-011078/01.
 DR
 XX P-PSDB; AAR83015.

XX Oligo- and polynucleotide(s) that bind to lung cell nuclear proteins -
 PT useful for cancer diagnosis and therapy.
 PT
 XX Claim 50; Fig 39; 157pp; English.

XX This sequence encodes the thyroid transcription factor, TTF-1. This
 CC sequence was isolated from the human adenocarcinoma cell line H441. The
 CC TTF-1 locus is contained within a 4.6 kb BamHI fragment and consists of
 CC two exons and one intron. The predicted amino acid sequence of human TTF-

CC 1 shows close identity with the amino acid sequence predicted by the rat
 CC TTF-1 cDNA sequence and 92.4% identity with the rat TTF-1 cDNA. The
 CC intron is approx. 1 kb in length and is flanked by consensus splice donor
 CC -acceptor sites that fit splice acceptor-donor rules. The mRNA produced
 CC is 2.3 kb as detected by Northern blot analysis of mRNA derived from
 CC mouse and human adenocarcinoma cells. TTF-1 mRNA was detected in human
 CC pulmonary adenocarcinoma cells H461 and H620 and small cell carcinoma
 CC epithelial cell lines, A549, Hela or 3T3 cells, demonstrating the cell
 CC selectivity of TTF-1 expression. TTF-1 has been detected in nuclei of the
 CC respiratory epithelium in human fetal lungs as early as 11-12 weeks of
 CC gestation. Immunostaining has observed a distribution pattern in the
 CC developing airways similar to the for pro-SP-C. TTF-1 was detected in
 CC subsets of respiratory epithelial cells in the developing lung, including
 CC nonciliated bronchiolar, and rarely in nonciliated bronchial respiratory
 CC epithelial cells in the immature lung. At the time of birth TTF-1 was
 CC detected in alveolar Type II epithelial cells and in subsets of
 CC nonciliated bronchiolar epithelial cells. TTF-1 was not detected in
 CC alveolar Type I cells or ciliated epithelial cells. In the adult lung,
 CC TTF-1 is detected in subsets of nonciliated bronchiolar epithelial cells
 CC and was most prominent in type II epithelial cells but was excluded from
 CC Type I cells. Due to poor print quality in the specification, this
 CC sequence was obtained from GenBank HSU19816

XX Sequence 3293 BP; 676 A; 1003 C; 1020 G; 594 T; 0 U; 0 Other;

Query Match 80.0%; Score 19.2; DB 2; Length 3293;
 Best Local Similarity 87.5%; Pred. No. 59;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGGCTT 24
 |||||
 Db 2579 CCAGCAGTTTGGCCTTTGGCTT 2556

RESULT 12
 AAS11829/c
 ID AAS11829 standard; DNA; 3293 BP.

XX AAS11829;

DT 24-OCT-2001 (first entry)

XX Human TTF-1 gene.

DE Human; thyroid transcription factor; TTF-1; lung cancer; thyroid cancer;
 KW ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT exon 1..710

FT /*tag= a

FT /number= 1

FT 83

FT /*tag= b

FT /note= "The sequence is unreadable at this position"

FT 339..2517

FT /*tag= c

FT /product= "TTF-1"

FT 711..1674

FT /*tag= d

FT /number= 1

FT 1675..3293

FT /*tag= e

FT /number= 2

FT polyA_signal 3261..3266

FT /*tag= f

XX US2001016352-A1.

PN 23-AUG-2001.

XX XX

PF 26-MAY-1999; 99US-00320337.
 XX
 PR 18-MAY-1994; 94US-00245356.
 PR 17-MAY-1995; 95US-00442809.
 XX

PA (BOHI/) BOHINSKI R J.
 PA (WHIT/) WHITSETT J A.

PI Bohinski RJ, Whitsett JA;

DR WPI; 2001-513959/56.

DR P-PSDB; AAU05583.

XX Oligonucleotide sequences which bind nuclear proteins and surfactants
 PT found in lung cells, useful for detecting cancers that originate in the
 PT lung.

XX Example 7; Fig 39; 76pp; English.

XX The invention relates to an oligonucleotide which includes at least 1
 CC nucleic acid sequence which binds to at least 1 nuclear protein found in
 CC lung cells (e.g. the thyroid transcription factor 1, TTF-1, protein). The
 CC oligonucleotide can be expressed in lung cells via a vector and can be
 CC used to target therapeutic agents to kill lung or thyroid cancer cells.
 CC The oligonucleotide can be used to detect or diagnose lung or thyroid
 CC cancer. The oligonucleotides may be designed from the sequences of, for
 CC example, the promoters of lung-specific genes such as those encoding
 CC surfactant proteins. The present sequence is the human thyroid
 CC transcription factor gene, TTF-1

XX Sequence 3293 BP; 676 A; 1021 C; 1002 G; 593 T; 0 U; 1 Other;

Query Match 80.0%; Score 19.2; DB 4; Length 3293;

Best Local Similarity 87.5%; Pred. No. 59;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGGCTT 24

|||||
 Db 2579 CCAGCAGTTTGGCCTTTGGCTT 2556

RESULT 13

ADQ56478/c

ID ADQ56478 standard; DNA; 473 BP.

XX ADQ56478;

XX 21-OCT-2004 (first entry)

XX Novel canine microarray-related DNA sequence SeqID7780.

XX canine microarray; drug screening; toxicity assay;
 KW environmental pollutant; cellular response; gene expression profile;
 KW toxic response; liver necrosis; fatty liver disease;
 KW protein adduct formation; hepatitis; dog; ds.

XX Canis familiaris.

XX WO2004063324-A2.

XX 29-JUL-2004.

XX 05-MAY-2003; 2003WO-US013853.

XX 03-MAY-2002; 2002US-0377240P.

XX (GENE-) GENE LOGIC INC.

XX (PFIZ) PFIZER PROD INC.

XX Diggins JC, Porter M, Wei T;

XX WPI; 2004-561890/54.

XX XX

PT New isolated nucleic acid molecule, useful for drug screening and
PT toxicity assays or for assessing the impact, including toxicity, of a
PT compound, pharmaceutical agent or environmental pollutant on a cell or
PT living organism.
XX
XX Claim 1; SEQ ID NO 7780; 41pp; English.
XX
XX This invention is related to a novel isolated canine nucleic acid
CC sequences and the construction of canine microarrays containing a
CC significant portion of the canine genome. The isolated canine nucleic
CC acid sequences of the invention may be useful for drug screening and
CC toxicity assays. The invention is therefore useful for assessing the
CC impact, including toxicity, of a compound, pharmaceutical agent or
CC environmental pollutant on a cell or living organism. The methods are
CC useful for detecting genes that are up- or down-regulated in canines in a
CC disease state. The sequences are useful as diagnostic agents or markers
CC to detect a cellular response in a sample individually or as part of a
CC gene expression profile. It is also useful as a target for agents that
CC modulate gene expression or activity. The database is useful for
CC producing electronic Northern blots that allow the user to determine the cell
CC type or tissue in which a given gene is expressed and to allow
CC determination of the abundance or expression level of a given gene in a
CC particular tissue or cell. The methods are useful for determining the
CC similarity of a toxic response to one or more individual compounds. The
CC methods are useful for predicting at least one toxic response or the
CC likelihood that a compound or test agent will induce various specific
CC pathologies such as those of the liver (liver necrosis, fatty liver
CC disease, protein aduct formation or hepatitis), those of the kidney,
CC heart, brain or testes, or other pathologies associated with at least one
CC of the toxins. The methods are also useful for predicting or elucidating
CC the potential cellular pathways influenced, induced or modulated by the
CC compound or test agent due to the similarity of the expression profile
CC compared to the profile induced by a known toxin. The present sequence is
CC that of a canine DNA sequence which was claimed for use during the
CC production of a canine microarray of the invention.
XX
XX SQ Sequence 473 BP; 181 A; 77 C; 105 G; 110 T; 0 U; 0 Other;
Query Match 76.7%; Score 18.4; DB 13; Length 473;
Best Local Similarity 95.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 5 TAGTTAGCCTTTGGCTT 24
Db 308 TTGTTAGCCTTTGGCTT 289
RESULT 14
ADK16180/c
ID ADK16180 standard; DNA; 621 BP.
XX
XX AC ADK16180;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Nanoarchaeum equitans cancer-associated (CA) gene #66.
XX
XX KW cancer-associated gene; CA gene; cancer; carcinoma; lymphoma; leukaemia;
XX ds; gene.
XX
XX OS Nanoarchaeum equitans.
XX
XX PN WO2003093434-A2.
XX
XX PD 13-NOV-2003.
XX
XX PF 01-MAY-2003; 2003WO-US013699.
XX
XX PR 01-MAY-2002; 2002US-0377447P.
XX
XX PA (DIVE-) DIVERSA CORP.
XX
XX PI Stetter KO, Waters E, Kretz K, Podar M, Richardson T;
XX

PI Noordewier M;
XX WPI; 2004-053041/05.
DR P-PSDB; ADK16181.
XX
XX PT New recombinant cancer-associated genes, such as KCNJ9, useful for
PT diagnosing or treating carcinoma, e.g. breast, colon, rectal, pancreatic,
PT cervical, or skin cancers, lymphomas, or leukemia.
XX
XX PS Claim 5; SEQ ID NO 132; 251pp; English.
XX
XX CC The invention comprises then amino acid and coding sequences of cancer-
CC associated (CA) genes isolated from Nanoarchaeum equitans. The invention
CC also comprises the Nanoarchaeum equitans genome. The DNA and protein
CC sequences of the invention are useful for diagnosing and treating cancer
CC (e.g. carcinoma, lymphoma, or leukaemia). The present DNA sequence
CC represents a Nanoarchaeum equitans CA gene of the invention.
XX
XX SQ Sequence 621 BP; 232 A; 81 C; 86 G; 222 T; 0 U; 0 Other;
Query Match 75.8%; Score 18.2; DB 12; Length 621;
Best Local Similarity 87.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 CCAGTAGTTAGCCTTTGGCTT 23
Db 193 CGAATAGTTAGCCTTTGGCTT 171
RESULT 15
ADK16049 0
WP Sequence split into 5 fragments LOCUS ADK16049 Accession Adk16049
WP Fragment Name Begin End
WP ADK16049 0 1 110000
WP ADK16049 1 100001 210000
WP ADK16049 2 200001 310000
WP ADK16049 3 300001 410000
WP ADK16049 4 400001 490885
ID ADK16049 standard; DNA; 490885 BP.
XX
XX AC ADK16049;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Nanoarchaeum equitans genome.
XX
XX KW cancer-associated gene; CA gene; cancer; carcinoma; lymphoma; leukaemia;
XX ds.
XX
XX OS Nanoarchaeum equitans.
XX
XX PN WO2003093434-A2.
XX
XX PD 13-NOV-2003.
XX
XX PF 01-MAY-2003; 2003WO-US013699.
XX
XX PR 01-MAY-2002; 2002US-0377447P.
XX
XX PA (DIVE-) DIVERSA CORP.
XX
XX PI Stetter KO, Waters E, Kretz K, Podar M, Richardson T;
XX Noordewier M;
XX WPI; 2004-053041/05.
XX
XX PT New recombinant cancer-associated genes, such as KCNJ9, useful for
PT diagnosing or treating carcinoma, e.g. breast, colon, rectal, pancreatic,
PT cervical, or skin cancers, lymphomas, or leukemia.
XX
XX PS Claim 5; SEQ ID NO 1; 251pp; English.
XX
XX CC The invention comprises then amino acid and coding sequences of cancer-

associated (CA) genes isolated from Nanoarchaeum equitans. The invention also comprises the Nanoarchaeum equitans genome. The DNA and protein sequences of the invention are useful for diagnosing and treating cancer (e.g. carcinoma, lymphoma, or leukaemia). The present DNA sequence represents the Nanoarchaeum equitans genome.

SQ Sequence 490885 BP; 167981 A; 77361 C; 77560 G; 167983 T; 0 U; 0 Other;

Query Match	75.8%	Score 18.2;	DB 12;	Length 110000;
Best Local Similarity	87.0%	Pred. No. 2.7e+02;		
Matches 20; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy 1 CCAGTAGTTTAGCCTTGTGGCT 23
 | | | | | | | | | | | |
Db 60873 CGAATAGTTTAGCCTTGTGCT 60895

Search completed: July 20, 2005, 17:31:40
Job time : 225.652 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 16:53:52 ; Search time 75.6522 Seconds
(without alignments)
519.095 Million cell updates/sec

Title: US-10-041-030-8

Perfect score: 24

Sequence: 1 ccagtagttagccttggctt 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfileseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19.2	80.0	3293	2	US-08-442-809A-75
C 2	19.2	80.0	6250	4	US-09-949-016-13222
C 3	17.6	73.3	601	4	US-09-949-016-128695
C 4	17.6	73.3	235064	4	US-09-949-016-15390
C 5	17.4	72.5	205163	4	US-09-949-016-17009
C 6	17.2	71.7	601	4	US-09-949-016-158916
C 7	17.2	71.7	601	4	US-09-949-016-158917
C 8	17.2	71.7	601	4	US-09-949-016-158918
C 9	17.2	71.7	62354	4	US-09-949-016-16188
C 10	16.8	70.0	601	4	US-09-949-016-202241
C 11	16.8	70.0	790	1	US-08-306-691B-47
C 12	16.8	70.0	790	5	PCT-US93-06251-93
C 13	16.8	70.0	51161	4	US-09-949-016-17416
C 14	16.8	70.0	85869	4	US-09-949-016-12017
C 15	16.8	70.0	85878	4	US-09-949-016-16321
C 16	16.8	70.0	102304	4	US-09-949-016-12589
C 17	16.8	70.0	147382	4	US-09-949-016-14624
C 18	16.6	69.2	487	4	US-09-621-976-10207
C 19	16.6	69.2	1011	4	US-09-543-681A-1158
C 20	16.6	69.2	2004	4	US-09-252-991A-10609
C 21	16.6	69.2	2691	4	US-09-252-991A-10245
C 22	16.6	69.2	5976	3	US-08-621-944A-2
C 23	16.6	69.2	5976	3	US-08-945-567D-2
C 24	16.6	69.2	6429	4	US-09-540-236-1539
C 25	16.6	69.2	6973	1	US-08-478-370-1
C 26	16.6	69.2	6973	3	US-08-483-855C-1
C 27	16.6	69.2	6973	3	US-08-621-944A-1

C 28	16.6	69.2	6973	3	US-08-945-567D-1
C 29	16.6	69.2	6975	3	US-08-431-718C-1
C 30	16.6	69.2	9542	3	US-08-968-685A-9
C 31	16.6	69.2	62909	4	US-09-596-002-32
C 32	16.6	69.2	80269	4	US-09-949-016-15681
C 33	16.4	68.3	1680	4	US-09-328-352-1798
C 34	16.4	68.3	152486	4	US-09-949-016-12869
C 35	16.4	68.3	194933	4	US-09-949-016-14172
C 36	16.4	68.3	392000	4	US-10-027-983-11
C 37	16.2	67.5	223	4	US-09-549-848B-69
C 38	16.2	67.5	660	4	US-09-489-039A-4207
C 39	16.2	67.5	921	4	US-09-328-352-3953
C 40	16.2	67.5	1030	4	US-09-244-805-4
C 41	16.2	67.5	3630	3	US-09-221-017B-943
C 42	16.2	67.5	35100	2	US-08-770-379-18
C 43	16.2	67.5	35100	3	US-08-757-669A-18
C 44	16.2	67.5	35100	3	US-09-230-371A-18
C 45	16.2	67.5	44653	4	US-09-949-016-11944

ALIGNMENTS

RESULT 1

US-08-442-809A-75/c
; Sequence 75, Application US/08442809A
; Patent No. 5976873
; GENERAL INFORMATION:
; APPLICANT: Bohinski, Robert J.,
; APPLICANT: Whitsett, Jeffrey A.
; TITLE OF INVENTION: Nucleic Acid Sequences
; TITLE OF INVENTION: Controlling Lung Cell -
; TITLE OF INVENTION: Specific Gene Expression
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,809A
; FILING DATE: 17-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,356
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 271010-360
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3293 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
; NAME/KEY: human TTF-1 gene
; US-08-442-809A-75

Query Match 80.0%; Score 19.2; DB 2; Length 3293;

Best Local Similarity 87.5%; Pred. No. 9.8;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCAGTAGTATTAGCCTTTGTGGCTT 24
|||||
Db 2579 CCAGCAGTTTGGCCCTTTGTGGTTT 2556

```

RESULT 2
US-09-949-016-13222/c
Sequence 13222, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15390
LENGTH: 235064
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(235064)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15390

```

US-09-949-016-13222

Query Match	80.0%	Score 19,2	DB 4	Length 6250
Best Local Similarity	87.5%	Pred. No. 11		
Match 01. Conservative	0.	Mismatches 3	Indels 0	Gaps 0

Qy	1	CCAGTAGTTTAGCCTTGTGGCTT	24
Dh	4257	CCAGCAGTTTGGCCTTGTGGTTT	4234

```

RESULT 3
US-09-949-016-128695
; Sequence 128695, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIORITY APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128695
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-128695

```

Query Match	73.3%	Score 17.6;	DB 4;	Length 601;
Best Local Similarity	83.3%	Pred. No. 42;		
Matches	20:	Conservative	0:	Mismatches 4;
			Indels	0;
			Gaps	0;

QY 1 CCAGTAGTTAGCCTTTGTGGCTT 24

db 447 CCAGTTCTTGAGCCTTTGTGGATT 470

RESULT 4

```

US-09-949-016-15390
; Sequence 15390, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN
; TITLE OF INVENTION: WITH HUMAN DISEASE,
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15390
; LENGTH: 235064
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(235064)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15390

```

Query Match	73.3%;	Score 17.6;	DB 4;	Length 235064;
Best Local Similarity	83.3%;	Pred. No. 1.6e+02;		
Matches	20;	Mismatches	4;	Indels 0;
	Conservative			

QY 1 CCAGTAGTTTAGCCTTTGTGGCTT 24
|||
Db 185699 CCAGTCTTTGAGCCTTTGTGGATT 18

```

RESULT 5
US-09-949-016-17009/c
; Sequence 17009, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17009
; LENGTH: 205163
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17009

```

Query Match	72.5%;	Score 17.4;	DB 4;	Length 205163;
Best Local Similarity	94.7%;	Pred. No. 1.9e+02;		
Mismatches	18;	Conservative	0;	Indels 0;
		Mismatches 1;		

Qy 3 AGTAGTTAGCCTTGTGG 21
| | | | | | | | | |
nb 33884 AATAGTTAGCCTTGTGG 33866

RESULT 6
US-09-949-016-158916/c
; Sequence 158916, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158916
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-158916

Query Match 71.7%; Score 17.2; DB 4; Length 601;
Best Local Similarity 86.4%; Pred. No. 66;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGTGGCTT 24
||||| ||||||| |||||
Db 49 AGTAGTGTAGCCTTTTGGCGT 28

RESULT 7
US-09-949-016-158917/c
; Sequence 158917, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158917
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-158917

Query Match 71.7%; Score 17.2; DB 4; Length 601;
Best Local Similarity 86.4%; Pred. No. 66;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGTGGCTT 24
||||| ||||||| |||||
Db 329 AGTAGTGTAGCCTTTTGGCGT 308

RESULT 8
US-09-949-016-158918/c
; Sequence 158918, Application US/09949016

; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158918
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-158918

Query Match 71.7%; Score 17.2; DB 4; Length 601;
Best Local Similarity 86.4%; Pred. No. 66;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGTGGCTT 24
||||| ||||||| |||||
Db 445 AGTAGTGTAGCCTTTTGGCGT 424

RESULT 9
US-09-949-016-16188
; Sequence 16188, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16188
; LENGTH: 62354
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16188

Query Match 71.7%; Score 17.2; DB 4; Length 62354;
Best Local Similarity 86.4%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGTGGCTT 24
||||| ||||||| |||||
Db 22904 AGTAGTGTAGCCTTTTGGCGT 22925

RESULT 10
US-09-949-016-202241/c
; Sequence 202241, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 202241
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-202241

Query Match 70.0%; Score 16.8; DB 4; Length 601;
Best Local Similarity 90.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTAGTTAGCCTTTGTGG 21
||| ||||| ||||| |||||
Db 430 CAGGAGTTAGACTTTGTGG 411

RESULT 11
US-08-306-691B-47/c
Sequence 47, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5734039e
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 790 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-306-691B-47

Query Match 70.0%; Score 16.8; DB 1; Length 790;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 202241
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-202241

Query Match 70.0%; Score 16.8; DB 4; Length 601;
Best Local Similarity 90.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTAGTTAGCCTTTGTGG 21
||| ||||| ||||| |||||
Db 430 CAGGAGTTAGACTTTGTGG 411

RESULT 12
PCT-US93-06251-93/c
Sequence 93, Application PC/TUS9306251
GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 790 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-93

Query Match 70.0%; Score 16.8; DB 5; Length 790;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TAGTTAGCCTTTGTGGCTT 24
||| ||||| ||||| |||||
Db 73 TACTTTAGACTTTGTGGCTT 54

RESULT 13
US-09-949-016-17416/c
Sequence 17416, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 18:01:31 ; Search time 337.043 Seconds
(without alignments)
451.758 Million cell updates/sec

Title: US-10-041-030-8
Perfect score: 24
Sequence: 1 ccagtagtttagccttggctt 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues
Total number of hits satisfying chosen parameters: 14346486

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:
22: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:
24: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:
25: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
26: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
27: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	13	US-10-041-030-8
2	24	100.0	864	15	Sequence 8, Appli
3	24	100.0	3614	10	Sequence 1323, Ap
4	24	100.0	3615	10	Sequence 7043, Ap
5	24	100.0	3752	10	Sequence 7042, Ap
6	24	100.0	5579	14	Sequence 7041, Ap
7	24	100.0	5597	17	Sequence 135, App
					Sequence 287, App

8	24	100.0	5921	13	US-10-041-030-3
9	24	100.0	202802	17	US-10-085-117-286
10	19.2	80.0	2202	17	US-10-236-031B-25
11	19.2	80.0	3233	9	US-09-320-337-75
12	18.2	75.8	364	18	US-10-424-599-99303
13	18.2	75.8	143239	20	US-10-723-860-546
14	17.8	74.2	1931	13	US-10-027-632-254246
15	17.8	74.2	1931	13	US-10-027-632-254247
16	17.8	74.2	1931	13	US-10-027-632-254248
17	17.8	74.2	1931	13	US-10-027-632-254249
18	17.8	74.2	1931	13	US-10-027-632-254250
19	17.8	74.2	1931	13	US-10-027-632-254251
20	17.8	74.2	1931	17	US-10-027-632-254246
21	17.8	74.2	1931	17	US-10-027-632-254247
22	17.8	74.2	1931	17	US-10-027-632-254248
23	17.8	74.2	1931	17	US-10-027-632-254249
24	17.8	74.2	1931	17	US-10-027-632-254250
25	17.8	74.2	1931	17	US-10-027-632-254251
26	17.8	74.2	519599	22	US-10-737-082-73
27	17.8	74.2	519599	22	US-10-765-790-73
28	17.6	73.3	433	19	US-10-674-124A-19288
29	17.6	73.3	474	14	US-10-007-280A-60
30	17.6	73.3	549	13	US-10-001-870-7
31	17.6	73.3	593	19	US-10-767-701-6659
32	17.4	72.5	285	17	US-10-242-535A-45964
33	17.4	72.5	285	18	US-10-085-783A-45964
34	17.4	72.5	477	17	US-10-242-535A-58345
35	17.4	72.5	477	18	US-10-085-783A-58345
36	17.4	72.5	504	10	US-09-918-995-25534
37	17.4	72.5	2366	17	US-10-172-118-1506
38	17.2	71.7	15275	9	US-09-764-869-1475
39	17.2	71.7	15275	14	US-10-091-504-1475
40	17.2	71.7	15275	17	US-10-227-577-1475
41	17.2	71.7	106344	10	US-09-910-185-10
42	17.2	71.7	106344	17	US-10-188-359-155
43	16.8	70.0	514	17	US-10-264-049-1350
44	16.8	70.0	564	17	US-10-343-650A-119
45	16.8	70.0	807	18	US-10-343-650A-119

ALIGNMENTS

RESULT 1
US-10-041-030-8
Sequence 8, Application US/10041030
Publication No. US20020150934A1
GENERAL INFORMATION:
APPLICANT: Powers, Scott
APPLICANT: Mu, David
APPLICANT: Xiang, Phil
APPLICANT: Peng, Yue
TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Mammalian
FILE REFERENCE: 018781-006810US
CURRENT APPLICATION NUMBER: US/10/041,030
CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 60/259,502
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
OTHER INFORMATION: probe N63226QR to pellino 2' untranslated region
US-10-041-030-8

Query Match 100.0% Score 24; DB 13; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.15;

Thu Jul 21 09:13:23 2005

us-10-041-030-8.rnpb

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGGGCTT 24
 |||||
 Db 1 CCAGTAGTTAGCCTTTGGGCTT 24
 |||||

RESULT 2
 US-10-106-698-1323
 ; Sequence 1323, Application US/10106698
 ; Publication No. US20030109690A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
 ; FILE REFERENCE: PA005P1
 ; CURRENT APPLICATION NUMBER: US/10/106,698
 ; CURRENT FILING DATE: 2002-03-27
 ; PRIOR APPLICATION NUMBER: PCT/US00/26524
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: US 60/157,137
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: US 60/163,280
 ; PRIOR FILING DATE: 1999-11-03
 ; NUMBER OF SEQ ID NOS: 8564
 ; SOFTWARE: PatentIn Ver. 3.0
 ; SEQ ID NO 1323
 ; LENGTH: 864
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (815)..(815)
 ; OTHER INFORMATION: n equals a.t.g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (848)..(848)
 ; OTHER INFORMATION: n equals a.t.g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (862)..(862)
 ; OTHER INFORMATION: n equals a.t.g, or c
 ; OTHER INFORMATION: n equals a.t.g, or c
 US-10-106-698-1323

Query Match 100.0%; Score 24; DB 15; Length 864;
 Best Local Similarity 100.0%; Pred. No. 0.24; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGGGCTT 24
 |||||
 Db 260 CCAGTAGTTAGCCTTTGGGCTT 283
 |||||

RESULT 3
 US-09-764-891-7043
 ; Sequence 7043, Application US/09764891
 ; Publication No. US20030077808A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC006
 ; CURRENT APPLICATION NUMBER: US/09/764,891
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 10231
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7043
 ; LENGTH: 3614
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-891-7043

Query Match 100.0%; Score 24; DB 10; Length 3614;
 Best Local Similarity 100.0%; Pred. No. 0.29; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGGGCTT 24
 |||||
 Db 3012 CCAGTAGTTAGCCTTTGGGCTT 3035
 |||||

RESULT 4
 US-09-764-891-7042
 ; Sequence 7042, Application US/09764891
 ; Publication No. US20030077808A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC006
 ; CURRENT APPLICATION NUMBER: US/09/764,891
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 10231
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7042
 ; LENGTH: 3615
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-891-7042

Query Match 100.0%; Score 24; DB 10; Length 3615;
 Best Local Similarity 100.0%; Pred. No. 0.29; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGGGCTT 24
 |||||
 Db 3013 CCAGTAGTTAGCCTTTGGGCTT 3036
 |||||

RESULT 5
 US-09-764-891-7041
 ; Sequence 7041, Application US/09764891
 ; Publication No. US20030077808A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC006
 ; CURRENT APPLICATION NUMBER: US/09/764,891
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 10231
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7041
 ; LENGTH: 3752
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-891-7041

Query Match 100.0%; Score 24; DB 10; Length 3752;
 Best Local Similarity 100.0%; Pred. No. 0.3; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGGGCTT 24
 |||||
 Db 3013 CCAGTAGTTAGCCTTTGGGCTT 3036
 |||||

RESULT 6
 US-10-197-666A-135
 ; Sequence 135, Application US/10197666A
 ; Publication No. US20030092037A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ASAHI KASEI KABUSIKI KAISYA
 ; TITLE OF INVENTION: Elki phosphorylation related gene
 ; FILE REFERENCE: PH-1548US
 ; CURRENT APPLICATION NUMBER: US/10/197,666A
 ; CURRENT FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: JP 2001-218204
 ; PRIOR FILING DATE: 2001-07-18

;; PRIOR APPLICATION NUMBER: JP 2001-263450
;; PRIOR FILING DATE: 2001-08-31
;; PRIOR APPLICATION NUMBER: JP 2002-012176
;; PRIOR FILING DATE: 2002-01-21
;; PRIOR APPLICATION NUMBER: US 60/305,884
;; PRIOR FILING DATE: 2001-07-18
;; PRIOR APPLICATION NUMBER: US 60/316,304
;; PRIOR FILING DATE: 2001-09-04
;; PRIOR APPLICATION NUMBER: US 60/350,027
;; PRIOR FILING DATE: 2002-01-23
;; NUMBER OF SEQ ID NOS: 156
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 135
;; LENGTH: 5579
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (177)..(1436)
US-10-197-666A-135

Query Match 100.0%; Score 24; DB 14; Length 5579;
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGTGGCTT 24
|||||
DB 5062 CCAGTAGTTAGCCTTTGTGGCTT 5085

RESULT 7
US-10-085-117-287
;; Sequence 287, Application US/10085117
;; Publication No. US20030232334A1
;; GENERAL INFORMATION:
;; APPLICANT: Morris, David W.
;; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
;; FILE REFERENCE: 529452000121
;; CURRENT APPLICATION NUMBER: US/10/085,117
;; CURRENT FILING DATE: 2002-02-27
;; PRIOR APPLICATION NUMBER: US 09/798,586
;; PRIOR FILING DATE: 2001-03-02
;; NUMBER OF SEQ ID NOS: 361
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 287
;; LENGTH: 5597
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-085-117-287

Query Match 100.0%; Score 24; DB 17; Length 5597;
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGTGGCTT 24
|||||
DB 5062 CCAGTAGTTAGCCTTTGTGGCTT 5085

RESULT 8
US-10-041-030-3
;; Sequence 3, Application US/10041030
;; Publication No. US20020150934A1
;; GENERAL INFORMATION:
;; APPLICANT: Powers, Scott
;; APPLICANT: Mu, David
;; APPLICANT: Xiang, Phil
;; APPLICANT: Peng, Yue
;; APPLICANT: Tularik Inc.
;; TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Mammalian
;; FILE REFERENCE: Pellino Polypeptides and Polynucleotides
;; FILE REFERENCE: 018781-006810US

;; CURRENT APPLICATION NUMBER: US/10/041,030
;; CURRENT FILING DATE: 2001-12-28
;; PRIOR APPLICATION NUMBER: US-60/259,502
;; PRIOR FILING DATE: 2001-01-02
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 3
;; LENGTH: 5921
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (501)..(1763)
;; OTHER INFORMATION: human pellino 2
US-10-041-030-3

Query Match 100.0%; Score 24; DB 13; Length 5921;
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGTGGCTT 24
|||||
DB 5386 CCAGTAGTTAGCCTTTGTGGCTT 5409

RESULT 9
US-10-085-117-286
;; Sequence 286, Application US/10085117
;; Publication No. US20030232334A1
;; GENERAL INFORMATION:
;; APPLICANT: Morris, David W.
;; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
;; FILE REFERENCE: 529452000121
;; CURRENT APPLICATION NUMBER: US/10/085,117
;; CURRENT FILING DATE: 2002-02-27
;; PRIOR APPLICATION NUMBER: US 09/798,586
;; PRIOR FILING DATE: 2001-03-02
;; NUMBER OF SEQ ID NOS: 361
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 286
;; LENGTH: 202802
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-085-117-286

Query Match 100.0%; Score 24; DB 17; Length 202802;
Best Local Similarity 100.0%; Pred. No. 0.5; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGTGGCTT 24
|||||
DB 192286 CCAGTAGTTAGCCTTTGTGGCTT 192309

RESULT 10
US-10-236-031B-25/c
;; Sequence 25, Application US/10236031B
;; Publication No. US20030219760A1
;; GENERAL INFORMATION:
;; APPLICANT: Gordon, Gavin J.
;; APPLICANT: Jensen, Roderick V.
;; APPLICANT: Gullana, Steven R.
;; APPLICANT: Bueno, Raphael
;; TITLE OF INVENTION: Diagnostic and Prognostic Tests
;; FILE REFERENCE: B00801/70265 (JRV/JAV)
;; CURRENT APPLICATION NUMBER: US/10/236,031B
;; CURRENT FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: US 60/317,389
;; PRIOR FILING DATE: 2001-09-05
;; PRIOR APPLICATION NUMBER: US 60/407,431
;; PRIOR FILING DATE: 2002-08-30
;; NUMBER OF SEQ ID NOS: 102

```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 2202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-236-031B-25

Query Match      80.0%; Score 19.2; DB 17; Length 2202;
Best Local Similarity 87.5%; Pred. No. 53; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 3;

Db          1451 CCAGCAGTTGGCCTTTGTGGTTT 1428
              ||||| ||||| ||||| ||||| |||||
1 CCAGTAGTTTAGCCTTTGTGGCTT 24

RESULT 11
US-09-320-337-75/c
; Sequence 75, Application US/09320337
; Patent No. US20010016352A1
; GENERAL INFORMATION:
; APPLICANT: Bohinski, Robert J.,
; APPLICANT: Whitsett, Jeffrey A.
; TITLE OF INVENTION: Nucleic Acid Sequences Controlling
; TITLE OF INVENTION: Lung Cell - Specific Gene Expression
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM P160
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: MS WORD 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/320,337
; FILING DATE: 26-MAY-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/442,809
; FILING DATE: 17-MAY-1995
; APPLICATION NUMBER: 08/245,356
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 271010-447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-994-1700
; TELEFAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3293 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
; NAME/KEY: human TTF-1 gene
US-09-320-337-75

Query Match      80.0%; Score 19.2; DB 9; Length 3293;
Best Local Similarity 87.5%; Pred. No. 56; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 3;

Yq          1 CCAGTAGTTTAGCCTTTGTGGCTT 24
              ||||| ||||| ||||| ||||| |||||
2579 CCAGCAGTTGGCCTTTGTGGTTT 2556

RESULT 12
US-10-424-599-99303/c
; Sequence 99303, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)/B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 99303
; LENGTH: 364
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(364)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_60685C.1
US-10-424-599-99303

Query Match      75.8%; Score 18.2; DB 18; Length 364;
Best Local Similarity 87.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 3;

Qy          1 CCAGTAGTTTAGCCTTTGTGGCT 23
              ||||| ||||| ||||| ||||| |||||
244 CCAGTAGTTTGCCCTTTGTGGCT 222

RESULT 13
US-10-723-860-546
; Sequence 546, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 546
; LENGTH: 143239
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-546

Query Match      75.8%; Score 18.2; DB 20; Length 143239;
Best Local Similarity 87.0%; Pred. No. 2.8e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 3;

Qy          2 CAGTAGTTTAGCCTTTGTGGCTT 24
              ||||| ||||| ||||| ||||| |||||
31734 CAGTAATTTGCGCTTTGTGGCTT 31756

RESULT 14
US-10-027-632-254246
; Sequence 254246, Application US/10027632
; Publication No. US20020198371A1

```

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 254246
LENGTH: 1931
TYPE: DNA
ORGANISM: Human
US-10-027-632-254246

Query Match 74.2%; Score 17.8; DB 13; Length 1931;
Best Local Similarity 90.5%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAGTAGTTAGCCTTTGTGG 21
Db 1461 CCATAGTTAGCCTTTGTGG 1481

RESULT 15

US-10-027-632-254247
Sequence 254247, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 254247
LENGTH: 1931
TYPE: DNA
ORGANISM: Human
US-10-027-632-254247

Query Match 74.2%; Score 17.8; DB 13; Length 1931;
Best Local Similarity 90.5%; Pred. No. 2.4e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCAGTAGTTAGCCTTTGTGG 21
Db 1461 CCATAGTTAGCCTTTGTGG 1481
Search completed: July 20, 2005, 20:42:08
Job time : 340.043 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 11:59:56 ; Search time 929.739 Seconds
(without alignments)
1250.808 Million cell updates/sec

Title: US-10-041-030-8
Perfect score: 24
Sequence: 1 ccagtagtttagcctttgtgctt 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	6	AX686410 Sequence
2	24	100.0	1890	9	AK025208 Homo sapi
3	24	100.0	5579	6	BD190328 Elk1 phos
4	24	100.0	5597	9	AF302502 Homo sapi
5	24	100.0	5921	6	AX686405 Sequence
6	24	100.0	86794	2	AC016103 Homo sapi
7	24	100.0	164550	9	CNS01RHY
8	24	100.0	175988	9	CNS05TC7
9	24	100.0	198278	2	AC010097 Homo sapi
10	24	100.0	233753	2	AC137805 Homo sapi
11	19.4	80.8	437	5	AB101392 Haplochrom
12	19.4	80.8	236880	2	AC140762 Rattus no
13	19.4	80.8	247187	2	AC094928 Rattus no
14	19.2	80.0	165	9	AY083588 Macaca mu
15	19.2	80.0	204	11	G29853 human STS S
16	19.2	80.0	982	11	G26717 human STS S
17	19.2	80.0	2131	9	BC006221 Homo sapi
18	19.2	80.0	2202	9	U43203 Human thyro
19	19.2	80.0	2336	9	U33749 Human thyro

C 20	19.2	80.0	2407	5	AY549336	AY549336 Hyla gran
C 21	19.2	80.0	3293	6	AR083536	AR083536 Sequence
C 22	19.2	80.0	3293	9	HSU19816	U19816 Human thyro
C 23	19.2	80.0	166862	9	CNS01DTS	AL132857 Human chr
C 24	19.2	80.0	248188	10	AC118595	AC118595 Mus muscu
C 25	18.8	78.3	643	11	BV038649	BV038649 S212P6046
C 26	18.8	78.3	1736	9	AK091028	AK091028 Homo sapi
C 27	18.8	78.3	152666	10	AC131765	AC131765 Mus muscu
C 28	18.4	76.7	212822	2	AC080156	AC080156 Rattus no
C 29	18.4	76.7	224709	2	AC106153	AC106153 Rattus no
C 30	18.4	76.7	225030	10	AC107608	AC107608 Rattus no
C 31	18.4	76.7	241120	2	AC123458	AC123458 Rattus no
C 32	18.4	76.7	251208	2	AC096610	AC096610 Rattus no
C 33	18.4	76.7	271367	2	AC105467	AC105467 Rattus no
C 34	18.2	75.8	1060	5	AY549337	AY549337 Hyla quen
C 35	18.2	75.8	1518	5	AY549335	AY549335 Hyla fasc
C 36	18.2	75.8	2337	5	AY326055	AY326055 Hyla pict
C 37	18.2	75.8	2339	5	AY326054	AY326054 Hyla lanc
C 38	18.2	75.8	2393	5	AY549325	AY549325 Hyla cain
C 39	18.2	75.8	2417	5	AY549318	AY549318 Hyla andi
C 40	18.2	75.8	2418	5	AY549326	AY549326 Hyla cain
C 41	18.2	75.8	2418	5	AY549330	AY549330 Hyla cain
C 42	18.2	75.8	2420	5	AY549331	AY549331 Hyla cord
C 43	18.2	75.8	2420	5	AY549354	AY549354 Hyla rioj
C 44	18.2	75.8	2420	5	AY549360	AY549360 Hyla sp.
C 45	18.2	75.8	2421	5	AY549357	AY549357 Hyla semi

ALIGNMENTS

RESULT 1
AX686410
LOCUS AX686410
DEFINITION Sequence 8 from Patent WO02059611.
ACCESSION AX686410
VERSION AX686410.1 GI:29372148
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Powers,S., Mu,D., Xiang,P. and Peng,Y.
TITLE Diagnosis and treatment of cancer using mammalian pellino polypeptides and polynucleotides
JOURNAL Patent: WO 02059611-A 8 01-AUG-2002;
Tularik Inc. (US)
FEATURES
Location/Qualifiers
1..24
source
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide probe N63226QR to pellino 2 3'
untranslated region"

ORIGIN
Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAGTAGTTTAGCCTTTGTGGCTT 24
DB 1 CCAGTAGTTTAGCCTTTGTGGCTT 24
RESULT 2
AK025208
LOCUS AK025208
DEFINITION Homo sapiens cDNA: FLJ21555 fis, clone COL06351.
ACCESSION AK025208
VERSION AK025208.1 GI:10437673
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2
AUTHORS Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: flcdna@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286, Fax: 81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

FEATURES
source Location/Qualifiers
1. .1890
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="COL06351"
/tissue_type="colon"
/clone_lib="COL"
/notes="cloning vector pME18SPL3"
238. .633
/note="unnamed protein product"
/codon_start=1
/protein_id="BAB15084.1"
/db_xref="GI:10437674"
/translation="MSCHFFKGLAPLPHVYTGNCRPIISCLGLTLPMPASSPPEVKVP VMSYRNIFQLFMSFTKKKIQSGWSTLSIFLVRNLLIIGAAGSCMLQLSTFPLFG SAFSKKGYSPPCRVLRFLDFLPTVAQKN"

CDS
238. .633
/note="unnamed protein product"
/codon_start=1
/protein_id="BAB15084.1"
/db_xref="GI:10437674"
/translation="MSCHFFKGLAPLPHVYTGNCRPIISCLGLTLPMPASSPPEVKVP VMSYRNIFQLFMSFTKKKIQSGWSTLSIFLVRNLLIIGAAGSCMLQLSTFPLFG SAFSKKGYSPPCRVLRFLDFLPTVAQKN"

ORIGIN
Query Match 100.0%; Score 24; DB 9; Length 1890;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGGCTT 24
|||||
Db 1303 CCAGTAGTTAGCCTTTGGCTT 1326

RESULT 3
BD190328
LOCUS BD190328 5579 bp DNA linear PAT 17-JUL-2003
DEFINITION Elkl phosphorylation related gene.
ACCESSION BD190328
VERSION BD190328.1 GI:33000067
KEYWORDS WO 03008589-A/68.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Matsumoto, O., Matsuda, A., Nagano, Y. and Suzuki, N.
TITLE Elkl phosphorylation related gene
JOURNAL Patent: WO 03008589-A 68 30-JAN-2003;
ASAHI KASEI CORP, OSAMU MATSUZAKI, AKIO MATSUDA, YUKIKO NAGANO, NAOMI SUZUKI
COMMENT OS Homo sapiens (human)
PN WO 03008589-A/68
PD 30-JAN-2003

PF 15-JUL-2002 WO 2002JP007174
PR 18-JUL-2001 JP 01P 218204, 31-AUG-2001 JP 01P 263450 PR
21-JAN-2002 JP 02P 012176
PI OSAMU MATSUZAKI, AKIO MATSUDA, YUKIKO NAGANO, NAOMI SUZUKI PC
C12N15/54, C12N19/12, G01N33/50, G01N33/15, C07K16/40, A61K39/385, PC
A61K31/711
CC Elkl phosphorylation related gene
FH Key Location/Qualifiers
FT CDS (177). .(1436).
FEATURES
source Location/Qualifiers
1. .5579
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 24; DB 6; Length 5579;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGGCTT 24
|||||
Db 5062 CCAGTAGTTAGCCTTTGGCTT 5085

RESULT 4
AF302502
LOCUS AF302502 5597 bp mRNA linear PRI 05-JUL-2001
DEFINITION Homo sapiens pellino 2 (PELI2) mRNA, complete cds.
ACCESSION AF302502
VERSION AF302502.1 GI:10242352
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Resch, K., Jockusch, H. and Schmitt-John, T.
TITLE Assignment of homologous genes, Pel11/PEL11 and Pel12/PELI2, for the Pelle adaptor protein Pellino to mouse chromosomes 11 and 14 and human chromosomes 2p13.3 and 14q21, respectively, by physical and radiation hybrid mapping
JOURNAL Cytogenet. Cell Genet. 92 (1-2), 172-174 (2001)
MEDLINE 21203570
PUBMED 11306823
REFERENCE 2
AUTHORS Resch, K., Jockusch, H. and Schmitt-John, T.
TITLE Direct Submission
JOURNAL Submitted (05-SEP-2000) Developmental Biology and Molecular Pathology, University of Bielefeld, Universitaetsstrasse 25, Bielefeld, NRW 33615, Germany
FEATURES
source Location/Qualifiers
1. .5597
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1. .5597
/gene="PELI2"
177. .1439
/gene="PELI2"
/note="similar to Drosophila melanogaster Pellino"
/codon_start=1
/product="pellino 2"
/protein_id="AAG15390.1"
/db_xref="GI:10242353"
/translation="MFSEQEEHCAPNKPVKYGLVVLGYNGALPNQDGRKRRKSRFA LYKRPKANGVKPSTVHTTISGONTDEAOITOSTISRFACRIVCDRNEVYTFARIFAAG QVGRSTESPIDFVVTDTISGONTDEAOITOSTISRFACRIVCDRNEVYTFARIFAAG DSSNIFRGEKAAKWNPDGMDGLTTNGVLVMPHPRGGFTESQGVNREISVCCDGVY TURETRSAQQRGLVSTNVNLDGSLDLCGATLLWPTADGLFHTPTQKHTLALROE INARPPQCPVGLNTLAFPSINRKEVSEKQWYVLSCHGVHGVHNNHRSRSDTEANERE CPMCRVTGVPVWLGCAGFYVDAGPPTAFTPCGHVCSKSAKYSQIPLPHGTHA FHACPFCAQLVGEQNCIKLIFQGPID"

ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 5597;
 Best Local Similarity 100.0%; Pred. No. 0.76; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCTTTGGCTT 24

Db 5062 CCAGTAGTTAGCTTTGGCTT 5085

RESULT 5

AX586405 LOCUS AX586405 5921 bp DNA linear PAT 29-MAR-2003

DEFINITION Sequence 3 from Patent WO02059611.

ACCESSION AX586405

VERSION AX586405.1 GI:29372143

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArelano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferris, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heath, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehotzky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

TITLE

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArelano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferris, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heath, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehotzky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

TITLE

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArelano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferris, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heath, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehotzky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

TITLE

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArelano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferris, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heath, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehotzky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

TITLE

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

JOURNAL

* 16029 16893: contig of 865 bp in length
* 16894 16931: gap of 100 bp
* 16994 17861: contig of 868 bp in length
* 17862 17961: gap of 100 bp
* 17962 18856: contig of 895 bp in length
* 18857 18956: gap of 100 bp
* 18957 19822: contig of 866 bp in length
* 19823 19922: gap of 100 bp
* 19923 20840: contig of 918 bp in length
* 20841 20940: gap of 100 bp
* 20941 21855: contig of 915 bp in length
* 21856 21955: gap of 100 bp
* 21956 22811: contig of 856 bp in length
* 22812 22911: gap of 100 bp
* 22912 23825: contig of 914 bp in length
* 23826 23925: gap of 100 bp
* 23926 24837: contig of 912 bp in length
* 24838 24937: gap of 100 bp
* 24938 25848: contig of 911 bp in length
* 25849 25948: gap of 100 bp
* 25949 26846: contig of 898 bp in length
* 26847 26946: gap of 100 bp
* 26947 27844: contig of 898 bp in length
* 27845 27944: gap of 100 bp
* 27945 28802: contig of 858 bp in length
* 28803 28902: gap of 100 bp
* 28903 29817: contig of 915 bp in length
* 29818 29917: gap of 100 bp
* 29918 30805: contig of 888 bp in length
* 30806 31808: contig of 903 bp in length
* 31809 31908: gap of 100 bp
* 31909 32805: contig of 897 bp in length
* 32806 32905: gap of 100 bp
* 32906 33766: contig of 861 bp in length
* 33767 33866: gap of 100 bp
* 33867 34762: contig of 896 bp in length
* 34763 34862: gap of 100 bp
* 34863 35762: contig of 900 bp in length
* 35763 35862: gap of 100 bp
* 35863 36770: contig of 908 bp in length
* 36771 36870: gap of 100 bp
* 36871 37832: contig of 962 bp in length
* 37833 37932: gap of 100 bp
* 37933 38814: contig of 882 bp in length
* 38815 38914: gap of 100 bp
* 38915 39783: contig of 869 bp in length
* 39784 39883: gap of 100 bp
* 39884 40823: contig of 940 bp in length
* 40824 40923: gap of 100 bp
* 40924 41823: contig of 900 bp in length
* 41824 41923: gap of 100 bp
* 41924 42808: contig of 885 bp in length
* 42809 42908: gap of 100 bp
* 42909 43822: contig of 914 bp in length
* 43823 43922: gap of 100 bp
* 43923 44809: contig of 887 bp in length
* 44810 44909: gap of 100 bp
* 44910 45779: contig of 870 bp in length
* 45780 45879: gap of 100 bp
* 45880 46772: contig of 893 bp in length
* 46773 46872: gap of 100 bp
* 46873 47758: contig of 886 bp in length
* 47759 47858: gap of 100 bp
* 47859 48778: contig of 920 bp in length
* 48779 48879: gap of 100 bp
* 48880 49740: contig of 862 bp in length
* 49741 49840: gap of 100 bp
* 49841 50694: contig of 854 bp in length
* 50695 50794: gap of 100 bp
* 50795 51599: contig of 905 bp in length
* 51799 51999: gap of 100 bp
* 51800 52685: contig of 886 bp in length

* 52686 52785: gap of 100 bp
* 52786 53705: contig of 920 bp in length
* 53706 53805: gap of 100 bp
* 53806 54718: contig of 913 bp in length
* 54719 54818: gap of 100 bp
* 54819 55719: contig of 901 bp in length
* 55720 55819: gap of 100 bp
* 55820 56733: contig of 914 bp in length
* 56734 56833: gap of 100 bp
* 56834 57742: contig of 909 bp in length
* 57743 57842: gap of 100 bp
* 57843 58753: contig of 911 bp in length
* 58754 58853: gap of 100 bp
* 58854 59748: contig of 895 bp in length
* 59749 59848: gap of 100 bp
* 59849 60720: contig of 872 bp in length
* 60721 60820: gap of 100 bp
* 60821 61697: contig of 877 bp in length
* 61698 61797: gap of 100 bp
* 61798 62699: contig of 902 bp in length
* 62700 62799: gap of 100 bp
* 62800 63701: contig of 902 bp in length
* 63702 63801: gap of 100 bp
* 63802 64667: contig of 866 bp in length
* 64668 64767: gap of 100 bp
* 64768 65673: contig of 906 bp in length
* 65674 65773: gap of 100 bp
* 65774 66698: contig of 925 bp in length
* 66699 66798: gap of 100 bp
* 66799 67694: contig of 896 bp in length
* 67695 67794: gap of 100 bp
* 67795 68697: contig of 903 bp in length
* 68698 68797: gap of 100 bp
* 68798 69697: contig of 900 bp in length
* 69698 69797: gap of 100 bp
* 69798 70737: contig of 940 bp in length
* 70738 70837: gap of 100 bp
* 70838 71729: contig of 892 bp in length
* 71730 71829: gap of 100 bp
* 71830 72713: contig of 884 bp in length

Query Match 100.0%; Score 24; DB 2; Length 86794;

Best Local Similarity 100.0%; Pred. No. 0.54; Mismatches 0; Indels 0; Gaps 0;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGTGCTT 24

DB 13221 CCAGTAGTTAGCCTTTGTGCTT 13198

RESULT 7

CNS01RHY/c

LOCUS

DEFINITION

Human chromosome 14 DNA sequence BAC R-21008 of library RPCI-11

from chromosome 14 of Homo sapiens (Human), complete sequence.

ACCESSION

AL162633

VERSION

AL162633.3

KEYWORDS

HTG.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 164550)

Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P.,

Brottier, P., Catolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,

Levy, M., Eckenberg, R., Bruls, T., DeBerardinis, V., Cruaud, C.,

Gyapay, G., Saurin, W. and Weissbach, J.

Sequencing of the human chromosome 14

Unpublished

2 (bases 1 to 164550)

Genoscope.

Direct Submission

Title

Submitted (26-APR-2001) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Dec 4, 2000 this sequence version replaced gi:17799785.

COMMENT

Center: Genoscope / Centre National de Sequencage

Center code: GS

Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-930011
Downstream BAC (overlapping the SP6 end) : C-2184N20 (AC=AL359234)
----- Summary Statistics -----
Assembly program: Phrap; version 2.0
Quality coverage: 16.67x in Q20 bases; sum-of-contigs

Overall quality chart :

Range : bases

0 : 1 - 9 : 1

10 - 19 : 8

20 - 29 : 19

30 - 39 : 125

40 - 49 : 742

50 - 59 : 1376

60 - 69 : 1816

70 - 79 : 4694

80 - 89 : 21302

90 - 99 : 134467

Percentage of bases with a quality value >= 40 : 99 %.

FEATURES

source

1. 164550

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="14"

/clone_lib="RPCI-11"

142293..142420

/notes="matching EMBL:H53462"

RHdb:RH53794

dbSTS:STS6714

Identified using the e-PCR software (G. Schuler)"

STS

ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 164550;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTTACGCTTTGGCTT 24

Db 112410 CCAGTAGTTTACGCTTTGGCTT 112387

RESULT 8

CNS05TC7

LOCUS

DEFINITION

Human chromosome 14 DNA sequence BAC R-930011 of library RPCI-11

from chromosome 14 of Homo sapiens (Human), complete sequence.

ACCESSION AL355073

VERSION AL355073.5

KEYWORDS HTG.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 175988)

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P.,

Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,

Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C.,

Gyapay, G., Saurin, W. and Weissenbach, J.

Sequencing of the human chromosome 14

Unpublished

2 (bases 1 to 175988)

Genoscope.

Direct Submission

Submitted (26-APR-2001) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

On Apr 30, 2001 this sequence version replaced gi:12697154.

----- Genom Center -----

Center: Genoscope / Centre National de Sequencage

Center code: GS

Web site: http://www.genoscope.cns.fr/

Contact: SeqRef@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.

Upstream BAC (overlapping the T7 end) : C-2588E21

Downstream BAC (overlapping the SP6 end) : R-21008 (AC=AL162633)

----- Summary Statistics -----

Assembly program: Phrap; version 2.0

Quality coverage: 7.58x in Q20 bases; sum-of-contigs

Overall quality chart :

Range : bases

0 : 1 - 9 : 1

10 - 19 : 8

20 - 29 : 19

30 - 39 : 125

40 - 49 : 742

50 - 59 : 1376

60 - 69 : 1816

70 - 79 : 4694

80 - 89 : 21302

90 - 99 : 101037

Percentage of bases with a quality value >= 40 : 99 %.

Location/Qualifiers

1. 175988

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="14"

/clone_lib="RPCI-11"

72485..72612

/note="matching EMBL:H53462"

RHdb:RH53794

dbSTS:STS6714

Identified using the e-PCR software (G. Schuler)"

FEATURES

source

1. 175988

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="14"

/clone_lib="RPCI-11"

72485..72612

/note="matching EMBL:H53462"

RHdb:RH53794

dbSTS:STS6714

Identified using the e-PCR software (G. Schuler)"

STS

ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 175988;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTTACGCTTTGGCTT 24

Db 102488 CCAGTAGTTTACGCTTTGGCTT 102511

RESULT 9

AC010097/c

LOCUS

DEFINITION

Homo sapiens chromosome 14 clone RP11-378116, WORKING DRAFT

SEQUENCE, 18 unordered pieces.

ACCESSION AC010097

VERSION AC010097.6

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AC010097 198278 bp DNA linear HTG 07-JUL-2000

Homo sapiens chromosome 14 clone RP11-378116, WORKING DRAFT

SEQUENCE, 18 unordered pieces.

ACCESSION AC010097

VERSION AC010097.6

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 198278)
 Waterston, R.H.
 The sequence of Homo sapiens clone
 Unpublished
 2 (bases 1 to 198278)
 Waterston, R.H.
 Direct Submission
 Submitted (11-SEP-1999) Genome Sequencing Center, Washington
 University School of Medicine, 444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Jul 7, 2000 this sequence version replaced gi:8568179.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc/index.shtml>
 ----- Project Information -----
 Center project name: H.NH0378116
 ----- Summary Statistics -----
 Sequencing vector: M13; 88%
 Sequencing vector: plasmid; 12%
 Chemistry: Dye-primer ET; 73% of reads
 Assembly: Dye-terminator Big Dye; 27% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 191558 bases at least Q40
 Consensus quality: 193468 bases at least Q30
 Consensus quality: 194761 bases at least Q20
 Insert size: 195000; agarose-fp
 Insert size: 196578; sum-of-contigs
 Quality coverage: 5.76 in Q20 bases; agarose-fp
 Quality coverage: 5.18 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 18 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.
 *
 * 1 1211: contig of 1211 bp in length
 * 1212 1311: gap of unknown length
 * 1312 2946: contig of 1635 bp in length
 * 2947 3046: gap of unknown length
 * 3047 6236: contig of 3190 bp in length
 * 6237 6336: gap of unknown length
 * 6337 9363: contig of 3027 bp in length
 * 9364 9463: gap of unknown length
 * 9464 13995: contig of 4532 bp in length
 * 13996 14095: gap of unknown length
 * 14096 17948: contig of 3853 bp in length
 * 17949 18048: gap of unknown length
 * 18049 23265: contig of 5217 bp in length
 * 23266 23365: gap of unknown length
 * 23366 30448: contig of 7083 bp in length
 * 30449 30548: gap of unknown length
 * 30549 41508: contig of 10960 bp in length
 * 41509 51502: contig of 9894 bp in length
 * 51503 51602: gap of unknown length
 * 51603 61316: contig of 9714 bp in length
 * 61317 72947: contig of 11531 bp in length
 * 72948 73047: gap of unknown length
 * 73048 87327: contig of 14280 bp in length
 * 87328 87427: gap of unknown length
 * 87428 103771: contig of 16344 bp in length
 * 103772 103871: gap of unknown length
 * 103872 120942: contig of 17071 bp in length
 * 120943 121042: gap of unknown length
 * 121043 138875: contig of 17833 bp in length
 * 138876 138975: gap of unknown length

* 138976 162621: contig of 23646 bp in length
 * 162622 162721: gap of unknown length
 * 162722 198278: contig of 35557 bp in length.
 FEATURES
 source
 Location/Qualifiers
 1..198278
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="14"
 /clone="RP11-378116"
 ORIGIN
 Query Match 100.0% Score 24; DB 2; Length 198278;
 Best Local Similarity 100.0%; Pred.No. 0.49; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0;
 Oy 1 CCAAGTAGTTAGCCTTTGCGCTT 24
 ||||||||||||||||||
 Db 106197 CCAAGTAGTTAGCCTTTGCGCTT 106174
 ||||||||||||||||||
 RESULT 10
 AC137805/c
 LOCUS
 DEFINITION Homo sapiens chromosome 16 clone RP11-863C20, WORKING DRAFT
 AC137805 233753 bp DNA linear HTG 03-DEC-2002
 SEQUENCE, 2 unordered pieces.
 ACCESSION AC137805
 VERSION AC137805.1 GI:26006547
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 233753)
 DOE Joint Genome Institute.
 TITLE
 Sequencing of Human Chromosome 16
 JOURNAL
 Unpublished
 2 (bases 1 to 233753)
 DOE Joint Genome Institute.
 REFERENCE
 AUTHORS
 TITLE
 Direct Submission
 JOURNAL
 Submitted (03-DEC-2002) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: <http://www.jgi.doe.gov>

 Project Information
 Center Project Name: 1625964
 Center clone name: RPCI-11_863C20

 Summary Statistics
 Consensus quality: 233513 bases at least Q40
 Consensus quality: 233587 bases at least Q30
 Consensus quality: 233607 bases at least Q20
 Estimated insert size: 160000; agarose-fp estimation
 Estimated insert size: 233653; sum-of-contigs estimation
 Quality coverage: 18.97 in Q20 bases; agarose-fp estimation
 Quality coverage: 12.99 in Q20 bases; sum-of-contigs estimation.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.
 *
 * 1 23031: contig of 23031 bp in length
 * 23032 23131: gap of unknown length
 * 23132 233753: contig of 210622 bp in length.
 FEATURES
 source
 Location/Qualifiers
 1..233753
 /organism="Homo sapiens"

ORIGIN

Query Match 100.0%; Score 24; DB 2; Length 233753;
 Best Local Similarity 100.0%; Pred. No. 0.48; 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 CCAGTAGTTAGCCTTTGGCTT 24
 |||
 Db 131315 CCAGTAGTTAGCCTTTGGCTT 131292

HTG: HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
 Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

RESULT 11

AB101392

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 236880)
 Muzny, D., Maric, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,
 Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
 Anyalebech, V., Ayoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
 Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
 Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
 Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
 Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
 Cleveland, C., Cockrell, R., Cox, C., Coyne, M., Cree, A., D'Souza, L.,
 Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
 Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
 Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
 Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falle, T., Fan, G.,
 Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
 Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
 Gebrgeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
 Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
 Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
 Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hoques, M.,
 Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
 Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
 Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
 Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
 Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
 Lorensuwa, L., Loulaeged, H., Lozano, R. J., Lu, X., Ma, J.,
 Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
 Mangun, B., Mapua, P., Martin, K., Martin, R., Martine, E.,
 Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
 Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
 Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
 Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K.,
 Nwaekeme, O., Okwuonu, G., Olarnpunaagoon, A., Pal, S., Parks, K.,
 Pasernak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
 Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., L.,
 Puaio, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R.,
 Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, P.,
 Rivas, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,
 Sanders, W., Savery, G., Scherer, S., Scott, C., Shatman, S., Shen, H.,
 Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajls, D.,
 Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
 Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
 Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
 Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J.,
 Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, P.,
 Williams, G., Willson, R., Wiczysk, R., Wooden, H., Worley, K.,
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
 Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
 Weinstock, G. and Gibbs, R. A.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Direct Submission

Unpublished

2 (bases 1 to 236880)

Worley, K. C.

Direct Submission

Submitted (01-MAR-2003)

Of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 236880)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (13-MAY-2003)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:28626613.

The sequence in this assembly is a combination of BAC based reads

and whole genome shotgun sequencing reads assembled using Atlas

Qy 3 AGTAGTTAGCCTTTGGCTT 23
 |||
 Db 169 AGTTGTTAGCCTTTGGCTT 189

RESULT 12

AC140762

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 80.8%; Score 19.4; DB 5; Length 437;
 Best Local Similarity 95.2%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGGCTT 23
 |||
 Db 169 AGTTGTTAGCCTTTGGCTT 189

RESULT 12

AC140762

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 80.8%; Score 19.4; DB 5; Length 437;
 Best Local Similarity 95.2%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGGCTT 23
 |||
 Db 169 AGTTGTTAGCCTTTGGCTT 189

RESULT 12

AC140762

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 80.8%; Score 19.4; DB 5; Length 437;
 Best Local Similarity 95.2%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGGCTT 23
 |||
 Db 169 AGTTGTTAGCCTTTGGCTT 189

RESULT 12

AC140762

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 80.8%; Score 19.4; DB 5; Length 437;
 Best Local Similarity 95.2%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGGCTT 23
 |||
 Db 169 AGTTGTTAGCCTTTGGCTT 189

RESULT 12

AC140762

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 80.8%; Score 19.4; DB 5; Length 437;
 Best Local Similarity 95.2%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGGCTT 23
 |||
 Db 169 AGTTGTTAGCCTTTGGCTT 189

RESULT 12

AC140762

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 80.8%; Score 19.4; DB 5; Length 437;
 Best Local Similarity 95.2%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGGCTT 23
 |||
 Db 169 AGTTGTTAGCCTTTGGCTT 189

RESULT 12

AC140762

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 80.8%; Score 19.4; DB 5; Length 437;
 Best Local Similarity 95.2%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGGCTT 23
 |||
 Db 169 AGTTGTTAGCCTTTGGCTT 189

RESULT 12

AC140762

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 80.8%; Score 19.4; DB 5; Length 437;
 Best Local Similarity 95.2%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGGCTT 23
 |||
 Db 169 AGTTGTTAGCCTTTGGCTT 189

RESULT 12

AC140762

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 80.8%; Score 19.4; DB 5; Length 437;
 Best Local Similarity 95.2%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGGCTT 23
 |||
 Db 169 AGTTGTTAGCCTTTGGCTT 189

RESULT 12

AC140762

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 80.8%; Score 19.4; DB 5; Length 437;
 Best Local Similarity 95.2%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGGCTT 23
 |||
 Db 169 AGTTGTTAGCCTTTGGCTT 189

RESULT 12

AC140762

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 80.8%; Score 19.4; DB 5; Length 437;
 Best Local Similarity 95.2%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGGCTT 23
 |||
 Db 169 AGTTGTTAGCCTTTGGCTT 189

RESULT 12

AC140762

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 80.8%; Score 19.4; DB 5; Length 437;
 Best Local Similarity 95.2%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGGCTT 23
 |||
 Db 169 AGTTGTTAGCCTTTGGCTT 189

RESULT 12

AC140762

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 80.8%; Score 19.4; DB 5; Length 437;
 Best Local Similarity 95.2%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGTAGTTAGCCTTTGGCTT 23
 |||
 Db 169 AGTTGTTAGCCTTTGGCTT 189

RESULT 12

AC140762

LOCUS

DEFINITION

ACCESSION

VERSION

(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

```

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GKBZ
Center clone name: CH230-70P5
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 207907 bases at least Q40
Consensus quality: 211702 bases at least Q30
Consensus quality: 214041 bases at least Q20
Estimated insert size: 216628; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
*
* 1 234297: contig of 234297 bp in length
* 234298 234397: gap of unknown length
* 234398 235412: contig of 1015 bp in length
* 235413 235512: gap of unknown length
* 235513 236880: contig of 1368 bp in length.
FEATURES             Location/Qualifiers
source               1..236880
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-70P5"
misc_feature         1..990
                     /note="wgs_contig"
ORIGIN
Query Match          80.8%; Score 19.4; DB 2; Length 236880;
Best Local Similarity 95.2%; Pred. No. 84;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 CCAGTAGTTAGCCTTTGTGG 21
    |||||
Db 11172 CCAGTAGTTAGCCTTTGTGG 11192

```

```

RESULT 13
AC094928
LOCUS
DEFINITION
Rattus norvegicus clone CH230-6D14, WORKING DRAFT SEQUENCE, 4
AC094928
AC094928.7 GI:30466913
VERSION
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS
Rattus norvegicus (Norway rat)
SOURCE
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

```

REFERENCE
AUTHORS

1 (bases 1 to 247187)
Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsebrook, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Guerra, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havliak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensheewa, L., Loulseghe, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, G., Nguyen, N., Norris, S., Nwakeleneh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, I., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajda, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Woodden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

Direct Submission
Unpublished
2 (bases 1 to 247187)
Worley, K. C.

Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 247187)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On May 9, 2003 this sequence version replaced gi:23264792. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence

contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GBTB
Center clone name: CH230-6D14
----- Summary Statistics

Assembly program: Atlas;
Consensus quality: 228892 bases at least Q40
Consensus quality: 231505 bases at least Q30
Consensus quality: 233248 bases at least Q20
Estimated insert size: 228978; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 241575: contig of 241575 bp in length
241576 241675: gap of unknown length
241676 242742: contig of 1067 bp in length
242743 242842: gap of unknown length
242843 244551: contig of 1709 bp in length
244552 244651: gap of unknown length
244652 247187: contig of 2536 bp in length.
----- Location/Qualifiers

1. 247187
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-6D14"
1. 1736
/note="wgs end extension
clone_end:Sp6"
complement(4508..5181)
clone="clone_boundary
clone_end:Sp6
site:EcoRI
end sequence:BH358097"
complement(232634..233337)
/note="clone_boundary
clone_end:T7
site:EcoRI
end sequence:BH358095"
234739..235881
/note="wgs end extension
clone_end:T7"
239927..241575
/note="wgs end extension
clone_end:T7"

FEATURES

Source
1. 247187
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-6D14"
1. 1736
/note="wgs end extension
clone_end:Sp6"
complement(4508..5181)
clone="clone_boundary
clone_end:Sp6
site:EcoRI
end sequence:BH358097"
complement(232634..233337)
/note="clone_boundary
clone_end:T7
site:EcoRI
end sequence:BH358095"
234739..235881
/note="wgs end extension
clone_end:T7"
239927..241575
/note="wgs end extension
clone_end:T7"

ORIGIN

Query Match 80.8%; Score 19.4; DB 2; Length 247187;
Best Local Similarity 95.2%; Pred. No. 84;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCTTTGGT 21
|||||
DB 136174 CCAGTAGTTAGCTTTGGT 136194

RESULT 14

AY083588/c
LOCUS 165 bp DNA linear PRI 16-APR-2002
Macaca mulatta thyroid transcription factor 1 (TTF1) gene, 3' UTR.
DEFINITION
ACCESSION AY083588
VERSION AY083588.1 GI:20159658
KEYWORDS
SOURCE
ORGANISM

Macaca mulatta (rhesus monkey)

Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.

1 (bases 1 to 165)

Construction of a targeted rhesus macaque microarray

Norgren,R.B. Jr., Zink,M.A., Jia,Y., Ojeda,S.R. and Spindel,E.R.

Unpublished

2 (bases 1 to 165)

Submitted (11-MAR-2002) Molecular and Cellular Biology Core, Oregon

Regional Primate Research Center, 505 NW 185th Avenue, Beaverton,

OR 97006, USA

OR 97006, USA

Location/Qualifiers

1. 165

/organism="Macaca mulatta"

/mol_type="genomic DNA"

/db_xref="taxon:9544"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

/product="thyroid transcription factor 1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

<1..>165

/gene="TTF1"

Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600

Protocol: Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer: MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from U33749
-- Washington University/Merck EST sequence.

FEATURES

source
1..204
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="14"
STS
1..204
primer_bind
1..20
primer_bind
complement(185..204)

ORIGIN

Query Match 80.0%; Score 19.2; DB 11; Length 204;
Best Local Similarity 87.5%; Pred. No. 2.5e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCAGTAGTTTAGCCTTTGTGGCTT 24
Db 77 CCAGCAGTTTGGCCTTTGTGGTTT 54

Search completed: July 20, 2005, 18:01:27
Job time : 934.739 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 11:59:56 ; Search time 852.261 Seconds
(without alignments)
1250.808 Million cell updates/sec

Title: US-10-041-030-7
Perfect score: 22
Sequence: 1 gatgctgaagtcgtctcattgg 22

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_btg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sbs.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	100.0	22	6	AX686409	Sequence
C 2	22	100.0	60	6	CQ543281	Sequence
C 3	22	100.0	5579	6	BD190328	Elk1 phos
C 4	22	100.0	5579	6	AF302502	Sequence
C 5	22	100.0	5921	6	AX686405	Sequence
C 6	22	100.0	86794	2	AC016103	Homo sapi
C 7	22	100.0	164550	9	CNS01RHY	Homo sapi
C 8	22	100.0	175988	2	CNS05TC7	Homo sapi
C 9	22	100.0	198278	2	AC010097	Homo sapi
C 10	22	100.0	233753	2	AC137805	Homo sapi
C 11	20.4	92.7	1890	9	AK025208	Homo sapi
C 12	17.8	80.9	539	8	HAN507474	Heterobas
C 13	17.8	80.9	549	8	HAN507473	Heterobas
C 14	17.8	80.9	550	8	HIN507471	Heterobas
C 15	17.8	80.9	566	8	HPA507469	Heterobas
C 16	17.8	80.9	688	8	AF173650	Beta vulg
C 17	17.8	80.9	163246	2	AC120248	Rattus no
C 18	17.8	80.9	174021	9	AL358612	Human DNA
C 19	17.8	80.9	178004	2	AL590070	Homo sapi

C 20	17.8	80.9	220052	5	BX927308	Zebrafish
C 21	17.8	80.9	247754	2	AC106199	Rattus no
C 22	17.8	80.9	249418	2	AC097209	Rattus no
C 23	17.4	79.1	134787	2	AL356692	Homo sapi
C 24	17.4	79.1	164529	2	AC079975	Homo sapi
C 25	17.4	79.1	172482	10	AC115060	Mus muscu
C 26	17.4	79.1	172753	9	AL359259	Human DNA
C 27	17.4	79.1	176671	2	AC080149	Homo sapi
C 28	17.4	79.1	203279	9	AL354826	Human DNA
C 29	17.2	78.2	579	6	AR557605	Sequence
C 30	17.2	78.2	867	1	AB014978	Pseudomon
C 31	17.2	78.2	1485	4	BTTP1G	B. taurus TN
C 32	17.2	78.2	2014	8	APU12757	U12757 Acer pseudo
C 33	17.2	78.2	2182	6	AX427149	Sequence
C 34	17.2	78.2	3369	9	HSM805437	Homo sapi
C 35	17.2	78.2	3911	9	HSM806334	Homo sapi
C 36	17.2	78.2	3992	9	HSM806209	Homo sapi
C 37	17.2	78.2	4130	6	BD191477	Secreted
C 38	17.2	78.2	4218	9	HSM806037	Homo sapi
C 39	17.2	78.2	4458	9	HSM806297	Homo sapi
C 40	17.2	78.2	4799	6	CQ843490	Sequence
C 41	17.2	78.2	4799	9	AK126472	Homo sapi
C 42	17.2	78.2	7167	1	AE011527	Leptospir
C 43	17.2	78.2	9217	9	AB095939	Homo sapi
C 44	17.2	78.2	10867	1	AE001594	Chlamydia
C 45	17.2	78.2	10871	1	AE002227	Chlamydia

ALIGNMENTS

RESULT 1
AX686409
LOCUS AX686409
DEFINITION Sequence 7 from Patent WO02059611.
ACCESSION AX686409
VERSION AX686409.1 GI:29372147
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Powers, S., Mu, D., Xiang, P. and Peng, Y.
TITLE Diagnosis and treatment of cancer using mammalian pellino polypeptides and polynucleotides
JOURNAL Patent: WO 02059611-A 7 01-AUG-2002;
Tularik Inc. (US)
FEATURES
Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32830"
/note="oligonucleotide probe N632260F to pellino 2 3'
untranslated region"

ORIGIN
Query Match 100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTCATTGG 22
DB 1 GATGCTGAAGTCGTCCTCATTGG 22

RESULT 2
CQ543281/c
LOCUS CQ543281
DEFINITION Sequence 12916 from Patent WO0210449.
ACCESSION CQ543281
VERSION CQ543281.1 GI:41509545
KEYWORDS Homo sapiens (human)
SOURCE

ORIGIN
Query Match 100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTCATTGG 22
DB 1 GATGCTGAAGTCGTCCTCATTGG 22

RESULT 2
CQ543281/c
LOCUS CQ543281
DEFINITION Sequence 12916 from Patent WO0210449.
ACCESSION CQ543281
VERSION CQ543281.1 GI:41509545
KEYWORDS Homo sapiens (human)
SOURCE

ORIGIN
Query Match 100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTCATTGG 22
DB 1 GATGCTGAAGTCGTCCTCATTGG 22

RESULT 2
CQ543281/c
LOCUS CQ543281
DEFINITION Sequence 12916 from Patent WO0210449.
ACCESSION CQ543281
VERSION CQ543281.1 GI:41509545
KEYWORDS Homo sapiens (human)
SOURCE

ORIGIN
Query Match 100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTCATTGG 22
DB 1 GATGCTGAAGTCGTCCTCATTGG 22

RESULT 2
CQ543281/c
LOCUS CQ543281
DEFINITION Sequence 12916 from Patent WO0210449.
ACCESSION CQ543281
VERSION CQ543281.1 GI:41509545
KEYWORDS Homo sapiens (human)
SOURCE

ORIGIN
Query Match 100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTCATTGG 22
DB 1 GATGCTGAAGTCGTCCTCATTGG 22

RESULT 2
CQ543281/c
LOCUS CQ543281
DEFINITION Sequence 12916 from Patent WO0210449.
ACCESSION CQ543281
VERSION CQ543281.1 GI:41509545
KEYWORDS Homo sapiens (human)
SOURCE

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
Patent: WO 0210449-A 12916 07-FEB-2002;
CompuGen Inc. (US)
FEATURES
source
1..60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 22; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTG 22
|||||
Db 60 GATGCTGAAGTCGTCCTCATTTG 39
|||||

RESULT 3
BD190328/c
LOCUS BD190328 5579 bp DNA linear PAT 17-JUL-2003
DEFINITION Elki phosphorylation related gene.
ACCESSION BD190328
VERSION BD190328.1 GI:33000067
KEYWORDS WO 03008589-A/68.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5579)
Matsuzaki,O., Matsuda,A., Nagano,Y. and Suzuki,N.
Elki phosphorylation related gene
Patent: WO 03008589-A 68 30-JAN-2003;
ASAHI KASEI CORP, OSAMU MATSUZAKI, AKIO MATSUDA, YUKIKO NAGANO, NAOMI SUZUKI
COMMENT OS Homo sapiens (human)
PN WO 03008589-A/68
PD 30-JAN-2003
PF 15-JUL-2002 WO 2002JP007174
PR 18-JUL-2002 JP 01P 218204,31-AUG-2001 JP 01P 263450 PR
PI OSAMU MATSUZAKI, AKIO MATSUDA, YUKIKO NAGANO, NAOMI SUZUKI PC
C12N15/54, C12N9/12, G01N33/50, G01N33/15, C07K16/40, A61K39/385, PC
A61K31/711
CC Elki phosphorylation related gene
FH Key Location/Qualifiers
FT CDS
1..5579
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 22; DB 6; Length 5579;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTG 22
|||||
Db 5135 GATGCTGAAGTCGTCCTCATTTG 5114
|||||

RESULT 4
AF102502/c
LOCUS AF102502 5597 bp mRNA linear PRI 05-JUL-2001
DEFINITION Homo sapiens pellino 2 (PELL2) mRNA, complete cds.
ACCESSION AF302502
VERSION AF302502.1 GI:10242352
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5597)
Resch,K., Jockusch,H. and Schmitt-John,T.
Assignment of homologous genes, Pelli1/PELL1 and Pelli2/PELL2, for
the Pelli adaptor protein pellino to mouse chromosomes 11 and 14
and human chromosomes 2p13.3 and 14q21, respectively, by physical
and radiation hybrid mapping
Cytogenet. Cell Genet. 92 (1-2), 172-174 (2001)
JOURNAL MEDLINE 21203570
PUBMED 11306823
REFERENCE 2 (bases 1 to 5597)
AUTHORS Resch,K., Jockusch,H. and Schmitt-John,T.
TITLE Direct Submision
JOURNAL Submitted (05-SEP-2000) Developmental Biology and Molecular
Pathology, University of Bielefeld, Universitaetsstrasse 25,
Bielefeld, NRW 33615, Germany
FEATURES
source
1..5597
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1..5597
/gene="PELL2"
177..1439
/gene="PELL2"
/feature="similar to Drosophila melanogaster Pellino"
/codon_start=1
/product="pellino 2"
/protein_id="AAG15390.1"
/db_xref="GI:10242353"
/translation="MFSQGEHCAPNKEPVKYGELVVLVNGALPNDGRGRKSRFA
LYKRPKANGVPSTVHVISTPOASKAISKQHSISYTLNRQTVVVEYTHDKDMDM
QVGRSTSPIDFVVVDTTIGSQNTDEAQTQSTISRACRIVCDRNEPYTARIFAAGF
DSSKNIFIGKAAKWNPDGHMDGLTTNGVLVMPHPRGGFTBESQGVVREISVCGDVI
TLRETRSAQQRGLVSESTNVLQDGLDLGATLLWRTADGLFHTPTQKHLELRQE
INARPCPGVGLNTLAFPSINRKEVVEEKQKVALSCGHVGHGHNWGHRSSTEANERE
CPMCTVGPVPLWLGCEAGFYVDAGPTFTPCGHVCSKSAKISQIPLPHGTHA
FHAACPFCACTQLVGEQNCIKLIFQPID"
ORIGIN
Query Match 100.0%; Score 22; DB 9; Length 5597;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTG 22
|||||
Db 5135 GATGCTGAAGTCGTCCTCATTTG 5114
|||||

RESULT 5
AX686405/c
LOCUS AX686405 5921 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 3 from Patent WO02059611.
ACCESSION AX686405
VERSION AX686405.1 GI:29372143
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Powers,S., Mu,D., Xiang,P. and Peng,Y.
Diagnosis and treatment of cancer using mammalian pellino
polypeptides and polynucleotides
Patent: WO 02059611-A 3 01-AUG-2002;
Tularik Inc. (US)
JOURNAL

```



```

FEATURES             source
1. .5921
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
501. .1763
/notes="unnamed protein product; human pellino 2"
/codon_start=1
/db_xref="GI:29372144"
/translation="MFSPGOEHCAPNKEPVKYGELVGLVNGALPNGDRGRKSRFA
LYKPKANGKVPSTVHVISPOASKALSCQGHISITLNRQNTVVVEYTHDKDIDMF
QVGRSTSPDVFVDTISGSDTEAQITQSTISRFACRIVCDRNEPYTARIFAAGF
DSSKNIIFLGKAAKKNPDGMDGLTTNGVLVHMPRGFTTEESQGVYREISVCGDYV
TLRETRAQGRKLVESITNVLQDGLIDLCATLLWRTADGLPHTPTQKHIEALROE
INAAPOCPVGLNTLAFPSINRKEVVEEKOPWAYLSCGHVGHVHNGHRSDDTEANERE
CPMCRVTGPVPLWLGCEAGFYVDAGPTTAFTPCGHVCSEKSNKYSQLPLPHGTHA
FHAACPATQLVGEQNCIKLIFQPID"

ORIGIN
Query Match      100.0%; Score 22; DB 6; Length 5921;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATCCTGAAGTCGTCATTGG 22
|||||
Db 5459 GATCCTGAAGTCGTCATTGG 5438

RESULT 6
AC016103
LOCUS
DEFINITION
Homo sapiens clone RP11-26H17, LOW-PASS SEQUENCE SAMPLING.
ACCESSION
AC016103
VERSION
AC016103.2 GI:9134395
KEYWORDS
HTG; HTGS_Phrase0.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 86794)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferrelira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Teeftaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (20-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6456211.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
----- Project name: L4637

```

Center clone name: 26_H_17

NOTE: This record contains 87 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

1 878: contig of 878 bp in length
 * 879: gap of 100 bp
 * 979: contig of 904 bp in length
 * 1883: gap of 100 bp
 * 1883: contig of 898 bp in length
 * 2880: gap of 100 bp
 * 2881: contig of 920 bp in length
 * 3901: gap of 100 bp
 * 4001: contig of 856 bp in length
 * 4857: gap of 100 bp
 * 5857: contig of 901 bp in length
 * 5858: gap of 100 bp
 * 6873: contig of 916 bp in length
 * 6874: gap of 100 bp
 * 6974: contig of 881 bp in length
 * 7855: gap of 100 bp
 * 8847: contig of 892 bp in length
 * 8847: gap of 100 bp
 * 9865: contig of 919 bp in length
 * 9866: gap of 100 bp
 * 9866: contig of 918 bp in length
 * 10884: gap of 100 bp
 * 10884: contig of 926 bp in length
 * 11909: gap of 100 bp
 * 12928: contig of 919 bp in length
 * 13028: gap of 100 bp
 * 13930: contig of 902 bp in length
 * 14030: gap of 100 bp
 * 14031: contig of 894 bp in length
 * 14924: gap of 100 bp
 * 15025: contig of 904 bp in length
 * 15928: gap of 100 bp
 * 16029: contig of 865 bp in length
 * 16893: gap of 100 bp
 * 16893: contig of 868 bp in length
 * 17861: gap of 100 bp
 * 17862: contig of 895 bp in length
 * 18957: gap of 100 bp
 * 18957: contig of 866 bp in length
 * 19823: gap of 100 bp
 * 19823: contig of 918 bp in length
 * 20840: gap of 100 bp
 * 20841: contig of 915 bp in length
 * 21856: gap of 100 bp
 * 21856: contig of 856 bp in length
 * 22812: gap of 100 bp
 * 22812: contig of 914 bp in length
 * 23826: gap of 100 bp
 * 23826: contig of 912 bp in length
 * 24838: gap of 100 bp
 * 24838: contig of 911 bp in length
 * 25849: gap of 100 bp
 * 25849: contig of 898 bp in length
 * 26847: gap of 100 bp
 * 26847: contig of 898 bp in length
 * 27845: gap of 100 bp
 * 27845: contig of 858 bp in length
 * 28803: gap of 100 bp
 * 28803: contig of 915 bp in length
 * 29817: gap of 100 bp

* 29918 30805: contig of 888 bp in length
* 30905: gap of 100 bp
* 31808: contig of 903 bp in length
* 31809 gap of 100 bp
* 31909 32805: contig of 897 bp in length
* 32805: gap of 100 bp
* 32966 33766: contig of 861 bp in length
* 33766: gap of 100 bp
* 33867 34762: contig of 896 bp in length
* 34763 34862: gap of 100 bp
* 34863 35762: contig of 900 bp in length
* 35763 35862: gap of 100 bp
* 35863 36770: contig of 908 bp in length
* 36771 36870: gap of 100 bp
* 36871 37832: contig of 962 bp in length
* 37833 37932: gap of 100 bp
* 37933 38814: contig of 882 bp in length
* 38815 38914: gap of 100 bp
* 38915 39783: contig of 869 bp in length
* 39784 39883: gap of 100 bp
* 39884 40823: contig of 940 bp in length
* 40824 40923: gap of 100 bp
* 40924 41823: contig of 900 bp in length
* 41824 41923: gap of 100 bp
* 41924 42808: contig of 885 bp in length
* 42809 42908: gap of 100 bp
* 42909 43823: contig of 914 bp in length
* 43823 43923: gap of 100 bp
* 43923 44809: contig of 887 bp in length
* 44810 44909: gap of 100 bp
* 44910 45779: contig of 870 bp in length
* 45780 45879: gap of 100 bp
* 45880 46772: contig of 893 bp in length
* 46773 46872: gap of 100 bp
* 46873 47758: contig of 886 bp in length
* 47759 47858: gap of 100 bp
* 47859 48778: contig of 920 bp in length
* 48779 48878: gap of 100 bp
* 48879 49740: contig of 862 bp in length
* 49741 49840: gap of 100 bp
* 49841 50694: contig of 854 bp in length
* 50695 50794: gap of 100 bp
* 50795 51699: contig of 905 bp in length
* 51700 51799: gap of 100 bp
* 51800 52685: contig of 886 bp in length
* 52686 52786: gap of 100 bp
* 52786 53706: contig of 920 bp in length
* 53706 53806: gap of 100 bp
* 53806 54718: contig of 913 bp in length
* 54719 54818: gap of 100 bp
* 54819 55719: contig of 901 bp in length
* 55720 55819: gap of 100 bp
* 55820 56733: contig of 914 bp in length
* 56734 56833: gap of 100 bp
* 56834 57742: contig of 909 bp in length
* 57743 57842: gap of 100 bp
* 57843 58753: contig of 911 bp in length
* 58754 58853: gap of 100 bp
* 58854 59748: contig of 895 bp in length
* 59749 59848: gap of 100 bp
* 59849 60720: contig of 872 bp in length
* 60721 60820: gap of 100 bp
* 60821 61697: contig of 877 bp in length
* 61698 61797: gap of 100 bp
* 61798 62699: contig of 902 bp in length
* 62700 62799: gap of 100 bp
* 62800 63701: contig of 902 bp in length
* 63702 63801: gap of 100 bp
* 63802 64667: contig of 866 bp in length
* 64668 64767: gap of 100 bp
* 64768 65673: contig of 906 bp in length
* 65674 65773: gap of 100 bp
* 65774 66698: contig of 925 bp in length

* 66599 66798: gap of 100 bp
* 66799 67694: contig of 896 bp in length
* 67695 67794: gap of 100 bp
* 67795 68697: contig of 903 bp in length
* 68698 68797: gap of 100 bp
* 68798 69697: contig of 900 bp in length
* 69698 69797: gap of 100 bp
* 69798 70737: contig of 940 bp in length
* 70738 70837: gap of 100 bp
* 70838 71729: contig of 892 bp in length
* 71730 71829: gap of 100 bp
* 71830 72713: contig of 884 bp in length

Query Match 100.0%; Score 22; DB 2; Length 86794;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTGTCTCATTTGG 22
|||||

Db 13148 GATGCTGAAGTGTCTCATTTGG 13169
|||||

RESULT 7

CNS01RHY

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CNS01RHY 164550 bp DNA linear PRI 26-APR-2001
Human chromosome 14 DNA sequence BAC R-21008 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.

AL162633

AL162633.3 GI:11545121

HTG.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 164550)

Heilig, R., Petit, J. L., Vico, V., Dasilva, C., Robert, C., Wincker, P.,

Brotier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,

Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C.,

Gyapay, G., Saurin, W. and Weissenbach, J.

Sequencing of the human chromosome 14

Unpublished

2 (bases 1 to 164550)

Genoscope.

Direct Submission

Submitted (26-APR-2001) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

On Dec 4, 2000 this sequence version replaced gi:7799785.

----- Genome Center

Center: Genoscope / Centre National de Sequencage

Center code: GS

Web site: http://www.genoscope.cns.fr/

Contact: SeqRef@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.

Upstream BAC (overlapping the T7 end) : R-930011

Downstream BAC (overlapping the SP6 end) : C-2184N20 (AC-AL359234)

----- Summary Statistics

Assembly program: Phrap; version 2.0

Quality coverage: 16.67x in Q20 bases; sum-of-contigs

Overall quality chart :

Range : bases

0 : 1

1 - 9 : 8

10 - 19 : 19

20 - 29 : 125

30 - 39 : 742

40 - 49 : 1376

50 - 59 : 1816

60 - 69 : 4694

70 - 79 : 4694

80 - 89 : 21302
90 - 99 : 134467

Percentage of bases with a quality value >= 40 : 99 %.

FEATURES

source
Location/Qualifiers
1. .164550
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="14"
/clone="R-21008"
/clone_lib="RPCI-11"
142293. .142420
/note="matching EMBL:H53462
RHdb:RH53794
dbSTS:STS6714
Identified using the e-PCR software (G. Schuler)"

STS

ORIGIN

Query Match 100.0%; Score 22; DB 9; Length 164550;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCTCATTGG 22
|||||
Db 112337 GATGCTGAAGTCGTCTCATTGG 112358

RESULT 8

CNS05TC7
LOCUS Human chromosome 14 DNA sequence BAC R-930011 of library RPCI-11
DEFINITION from chromosome 14 of Homo sapiens (Human), complete sequence.

ACCESSION AL355073
VERSION AL355073.5 GI:13897293
KEYWORDS HTG.

ORGANISM

Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P.,
Brottier, P., Cattolico, L., Barbe, V., Palletier, E., Artiguenave, F.,
Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C.,
Gyapay, G., Saurin, W. and Weissbach, J.
Sequencing of the human chromosome 14

TITLE

Unpublished
2 (bases 1 to 175988)
Genoscope.

REFERENCE

Direct Submission
Submitted (26-APR-2001) Genoscope - Centre National de Sequencage :
BP 131 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

TITLE

On Apr 30, 2001 this sequence version replaced gi:12697154.
----- Genom Center
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: seqref@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : C-2588E21
Downstream BAC (overlapping the SP6 end) : R-21008 (AC-AL162633)

----- Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 7.58x in Q20 bases; sum-of-contigs

Overall quality chart :
Range : bases
0 :
1 - 9 :
10 - 19 :

20 - 29 : 2
30 - 39 : 73
40 - 49 : 1732
50 - 59 : 6318
60 - 69 : 6755
70 - 79 : 14805
80 - 89 : 45266
90 - 99 : 101037

Percentage of bases with a quality value >= 40 : 99 %.

FEATURES

Location/Qualifiers
1. .175988
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="14"
/clone="R-930011"
/clone_lib="RPCI-11"
72485. .72612
/note="matching EMBL:H53462
RHdb:RH53794
dbSTS:STS6714
Identified using the e-PCR software (G. Schuler)"

STS

Query Match 100.0%; Score 22; DB 9; Length 175988;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1 GATGCTGAAGTCGTCTCATTGG 22
|||||
Db 102561 GATGCTGAAGTCGTCTCATTGG 102540

RESULT 9

AC010097
LOCUS Homo sapiens chromosome 14 clone RP11-378116, WORKING DRAFT
DEFINITION SEQUENCE, 18 unordered pieces.

ACCESSION AC010097.6 GI:8954335

VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.

KEYWORDS Homo sapiens (human)

SOURCE

Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 198278)
Waterston, R.H.

AUTHORS

The sequence of Homo sapiens clone

TITLE

Unpublished
2 (bases 1 to 198278)

REFERENCE

Waterston, R.H.
Direct Submission
Submitted (11-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

COMMENT

On Jul 7, 2000 this sequence version replaced gi:8568179.

----- Genom Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml

----- Project Information -----

Center project name: H_NH0378116

----- Summary Statistics -----

Sequencing vector: plasmid; 12x

Chemistry: Dye-terminator Big Dye; 27x of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 191558 bases at least Q40

Consensus quality: 193468 bases at least Q30

Consensus quality: 194761 bases at least Q20

Insert size: 195000; agarose-fp
 Insert size: 196578; sum-of-ctnigs
 Quality coverage: 5.76 in Q20 bases; agarose-fp
 Quality coverage: 5.18 in Q20 bases; sum-of-ctnigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 18 ctnigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the ctnigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1211: ctnig of 1211 bp in length
 * 1212 1311: gap of unknown length
 * 1312 2946: ctnig of 1635 bp in length
 * 2947 3046: gap of unknown length
 * 3047 6236: ctnig of 3190 bp in length
 * 6237 6336: gap of unknown length
 * 6337 9363: ctnig of 3027 bp in length
 * 9364 13995: gap of unknown length
 * 13996 14095: ctnig of 4532 bp in length
 * 14096 17948: gap of unknown length
 * 17949 18048: ctnig of 3853 bp in length
 * 18049 23265: ctnig of 5217 bp in length
 * 23266 23366: gap of unknown length
 * 23367 30448: ctnig of 7083 bp in length
 * 30449 30548: gap of unknown length
 * 30549 41508: ctnig of 10960 bp in length
 * 41509 41608: gap of unknown length
 * 41609 51502: ctnig of 9894 bp in length
 * 51503 51602: gap of unknown length
 * 51603 61316: ctnig of 9714 bp in length
 * 61317 61416: gap of unknown length
 * 61417 72947: ctnig of 11531 bp in length
 * 72948 73047: gap of unknown length
 * 73048 87327: ctnig of 14280 bp in length
 * 87328 87427: gap of unknown length
 * 87428 103771: ctnig of 16344 bp in length
 * 103772 103871: gap of unknown length
 * 103872 120942: ctnig of 17071 bp in length
 * 120943 121042: gap of unknown length
 * 121043 138875: ctnig of 17833 bp in length
 * 138876 138975: gap of unknown length
 * 138976 162621: ctnig of 23646 bp in length
 * 162622 162722: gap of unknown length
 * 162723 198278: ctnig of 35557 bp in length.

FEATURES

source
 1. .198278
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="14"
 /clone="RP11-378116"

ORIGIN

Query Match 100.0%; Score 22; DB 2; Length 198278;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCTCATTGG 22
 |||||
 Db 106124 GATGCTGAAGTCGTCTCATTGG 106145

RESULT 10

AC137805 AC137805 233753 bp DNA linear HTG 03-DEC-2002
 LOCUS Homo sapiens chromosome 16 clone RP11-863C20, WORKING DRAFT
 DEFINITION
 AC137805 AC137805
 ACCESSION
 VERSION AC137805.1 GI:26006547

KEYWORDS

SOURCE
 ORGANISM

REFERENCE

AUTHORS
 TITLE

JOURNAL
 REFERENCE

AUTHORS
 TITLE

JOURNAL
 COMMENT

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
 Homo sapiens (human)
 Homo sapiens

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 1 (bases 1 to 233753)
 DOE Joint Genome Institute.
 Sequencing of Human Chromosome 16
 Unpublished

2 (bases 1 to 233753)
 DOE Joint Genome Institute.
 Direct Submission

Submitted (03-DEC-2002) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 -----Genome Center
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: http://www.jgi.doe.gov

Project Information
 Center Project Name: 1625964
 Center clone name: RPCI-11_863C20

Summary Statistics
 Consensus quality: 233513 bases at least Q40
 Consensus quality: 233587 bases at least Q30
 Consensus quality: 233607 bases at least Q20
 Estimated insert size: 160000; agarose-fp estimation
 Estimated insert size: 233653; sum-of-ctnigs estimation
 Quality coverage: 18.97 in Q20 bases; agarose-fp estimation
 Quality coverage: 12.99 in Q20 bases; sum-of-ctnigs estimation.

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 ctnigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the ctnigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 23031: ctnig of 23031 bp in length
 * 23032 23131: gap of unknown length
 * 23132 233753: ctnig of 210622 bp in length.

FEATURES

source
 1. .233753
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="RP11-863C20"
 /clone_lib="RPCI human BAC library 11"

ORIGIN

Query Match 100.0%; Score 22; DB 2; Length 233753;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCTCATTGG 22
 |||||
 Db 131242 GATGCTGAAGTCGTCTCATTGG 131263

RESULT 11

AK025208/c AK025208 1890 bp mRNA linear PRI 13-SEP-2003
 LOCUS Homo sapiens cDNA: FLJ21555 fis, clone COL06351.
 DEFINITION
 ACCESSION AK025208
 VERSION AK025208.1 GI:10437673
 KEYWORDS oligo capping; fis (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1

[illegible]

TITLE Direct Submission
JOURNAL Submitted (10-SEP-2002) Maijala P.M., Applied Chemistry and Microbiology, University of Helsinki, P.O. Box 56, FIN-00014, FINLAND
FEATURES
source
1. .549
/organism="Heterobasidion araucariae"
/mol_type="genomic DNA"
/isolate="B1080"
/specific_host="Araucaria cunninghamii"
/db_xref="taxon:13564"
/country="Papua New Guinea"
1. .549
/gene="mnpla"
join(<1. .131,192. .313,373. .448,500. .>549)
/gene="mnpla"
/EC_number="1.11.1.13"
/function="lignin degradation"
/codon_start=1
/product="putative Mn-dependent peroxidase"
/protein_id="CAD47807.1"
/db_xref="GI:23304314"
/db_xref="GOA:Q8J1U3"
/db_xref="UniProt/TREMBL:Q8J1U3"
/translation="GGADGSIIVFSDIETNFHANNGIDEIVFEQKPFIAHNIITPGDF IQPAGATGVSNRCAPQLDFLLGRPVAPADLTVPPEFDSVDSILARFNDTGFNAA EVVALLASHTIAADKVDVTIPTG"
<1. .131
/gene="mnpla"
/number=1
132. .191
/gene="mnpla"
/number=1
192. .313
/gene="mnpla"
/number=2
314. .372
/gene="mnpla"
/number=2
373. .448
/gene="mnpla"
/number=3
449. .499
/gene="mnpla"
/number=3
500. .>549
/gene="mnpla"
/number=4
ORIGIN
Query Match 80.9%; Score 17.8; DB 8; Length 549;
Best Local Similarity 90.5%; Pred. No. 4.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GATGCTGAAGTCGTCTCATTTG 21
| | | | | | | | | | | | | | | | | | | | | |
Db 420 GCTGCTGAAGTCGTGCATTG 440
| | | | | | | | | | | | | | | | | | | | | |
RESULT 14
HIN507471 550 bp DNA linear PLN 19-JUN-2003
LOCUS Heterobasidion abietinum partial mnpla gene for putative
DEFINITION Mn-dependent peroxidase, exons 1-4, isolate B1166.
ACCESSION AJ507471
VERSION AJ507471.1 GI:23304309
KEYWORDS Mn-dependent peroxidase; mnpla gene.
SOURCE Heterobasidion abietinum
ORGANISM Heterobasidion abietinum
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Schizophyllaceae; Heterobasidion; Heterobasidion
annosum species complex.
REFERENCE 1

AUTHORS Maijala P.M., Harrington, T.C. and Raudaskoski, M.
TITLE A peroxidase gene family and gene trees in Heterobasidion and related genera
JOURNAL Mycologia 95 (2), 209-221 (2003)
REFERENCE 2 (bases 1 to 550)
AUTHORS Maijala P.M.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2002) Maijala P.M., Applied Chemistry and Microbiology, University of Helsinki, P.O. Box 56, FIN-00014, FINLAND
FEATURES
Location/Qualifiers
1. .550
/organism="Heterobasidion abietinum"
/mol_type="genomic DNA"
/isolate="B1166"
/specific_host="Abies alba"
/db_xref="taxon:207833"
/country="Bulgaria"
1. .550
/gene="mnpla"
join(<1. .131,192. .313,374. .449,501. .>550)
/gene="mnpla"
/EC_number="1.11.1.13"
/function="lignin degradation"
/codon_start=1
/product="putative Mn-dependent peroxidase"
/protein_id="CAD47805.1"
/db_xref="GI:23304310"
/db_xref="GOA:Q8J1T6"
/db_xref="UniProt/TREMBL:Q8J1T6"
/translation="GGADGSIIVFSDIETNFHANNGIDEIVFEQKPFIAHNIITPGDF IQPAGATGVSNRCAPQLDFLLGRPVAPADLTVPPEFDSVDSILARFNDTGFNAA EVVALLASHTIAADKVDVTIPTG"
<1. .131
/gene="mnpla"
/number=1
132. .191
/gene="mnpla"
/number=1
192. .313
/gene="mnpla"
/number=2
314. .373
/gene="mnpla"
/number=2
374. .449
/gene="mnpla"
/number=3
450. .500
/gene="mnpla"
/number=3
501. .>550
/gene="mnpla"
/number=4
ORIGIN
Query Match 80.9%; Score 17.8; DB 8; Length 550;
Best Local Similarity 90.5%; Pred. No. 4.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GATGCTGAAGTCGTCTCATTTG 21
| | | | | | | | | | | | | | | | | | | | | |
Db 421 GCTGCTGAAGTCGTGCATTG 441
| | | | | | | | | | | | | | | | | | | | | |
RESULT 15
HPA507469 566 bp DNA linear PLN 19-JUN-2003
LOCUS Heterobasidion parviporum partial mnpla gene for putative
DEFINITION Mn-dependent peroxidase, exons 1-4, isolate B146.
ACCESSION AJ507469
VERSION AJ507469.1 GI:23304305
KEYWORDS Mn-dependent peroxidase; mnpla gene.

```

ORIGIN
Query_Match      80.9%; Score 17.8; DB 8; Length 566;
Best Local Similarity 90.5%; Pred. No. 4.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1  GATGCTGGAAGTCGCTCAATTG 21
          | | | | | | | | | |
Db      421 GCTGCTGGAAGTCGCTCAATTG 441

```

Search completed: July 20, 2005, 18:01:22
Job time : 858.261 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 11:52:56 ; Search time 201.348 Seconds
(without alignments)
646.813 Million cell updates/sec

Title: US-10-041-030-7

Perfect score: 22

Sequence: 1 gatcgtgaagtcgtctcattgg 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 segs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	6	ABQ78313
2	22	100.0	60	6	ABN40168
3	22	100.0	259	8	ABZ18999
4	22	100.0	554	6	ABT10524
5	22	100.0	864	4	AAH34231
6	22	100.0	3614	4	AAU04355
7	22	100.0	3615	4	AAU04354
8	22	100.0	3752	4	AAU04353
9	22	100.0	5579	8	ACC42349
10	17.2	78.2	2182	6	ABA95158
11	17.2	78.2	2415	8	ACA45178
12	17.2	78.2	3634	8	ABX77573
13	17.2	78.2	4070	6	ABQ92052
14	17.2	78.2	4130	2	AAV62749
15	17.2	78.2	4799	12	ADG64976
16	17.2	78.2	110000	2	AAH91990_01
17	17	77.3	958	4	AAH71176
18	17	77.3	1581	5	AAH66619
19	17	77.3	349980	8	AAH68529
20	16.8	76.4	1770	8	ACA34475

C 21	16.8	76.4	24080	9	ADA02813	Ada02813 Mouse Egr
C 22	16.8	76.4	24080	10	ADB72551	Adb72551 Mouse Egr
C 23	16.8	76.4	24080	10	ADC85293	Adc85293 Mouse Egr
C 24	16.8	76.4	24080	12	ADM74408	Adm74408 Murine ca
C 25	16.8	76.4	110000	2	AAH42063_15	Continuation (16 o
C 26	16.4	74.5	24902	11	ACN44544	Acn44544 Mouse gen
C 27	16.2	73.6	160	4	ABA36278	Abas36278 Probe #14
C 28	16.2	73.6	204	12	ADL03150	Adl03150 DNA encod
C 29	16.2	73.6	480	4	ABA26398	Abas26398 Probe #48
C 30	16.2	73.6	610	10	ADK53863	Adk53863 Plant DNA
C 31	16.2	73.6	732	6	ABQ70068	Abq70068 Listeria
C 32	16.2	73.6	1001	3	AAH51151	Aah51151 Human ME1
C 33	16.2	73.6	1002	10	ADB69281	Adb69281 C. neofor
C 34	16.2	73.6	1340	6	AAH562696	Aah562696 cDNA sequ
C 35	16.2	73.6	1478	13	ADS48878	Ada48878 Bacterial
C 36	16.2	73.6	1761	10	ACF71856	Acf71856 Photorhab
C 37	16.2	73.6	1872	8	ACA30358	ACA30358 Prokaryot
C 38	16.2	73.6	2081	12	ADQ63289	Adq63289 Novel hum
C 39	16.2	73.6	2241	6	ABH54378	Abh54378 cDNA enco
C 40	16.2	73.6	3002	10	ADB68920	Adb68920 C. neofor
C 41	16.2	73.6	3242	10	ADA53331	Ada53331 Human cod
C 42	16.2	73.6	3903	13	ADR06611	Adr06611 Full leng
C 43	16.2	73.6	5142	6	ABH67815	Abh67815 Human rec
C 44	16.2	73.6	5292	6	ABZ11699	Abz11699 Human pol
C 45	16.2	73.6	5406	10	ADF82184	Adf82184 Leukaemia

ALIGNMENTS

RESULT 1

ABQ78313
ID ABQ78313 standard; DNA; 22 BP.

XX ABQ78313;

XX 05-NOV-2002 (first entry)

XX Probe N63226QF to detect Pellino 2 gene in cancer cells.

XX Pellino 2; cancer; Pellino 1; cancer treatment; epithelial cancer;

XX Gastrointestinal tract cancer; probe; as.

XX Homo sapiens.

XX WO200259611-A2.

XX 01-AUG-2002.

XX 28-DEC-2001; 2001WO-US051368.

XX 02-JAN-2001; 2001US-0259502P.

XX (TULA-) TULARIK INC.

XX Powers S, Mu D, Xiang P, Peng Y;

XX WPI; 2002-619185/66.

XX Detecting cancer cells in mammalian sample, useful for identifying inhibitors for treating cancer e.g. epithelial cancer, comprises detecting an overexpression of, or increase in copy number of genes encoding, Pellino 1 and Pellino 2.

XX Example 2; Page 55; 69pp; English.

XX Probes ABQ78313-15 were used to detect human Pellino 2 gene in cancer cells. The specification describes a method for detecting cancer cells in biological sample from a mammal. The method comprises detecting an overexpression of, or increase in copy number of genes encoding, polypeptides Pellino 1 or Pellino 2. The method is useful in detecting cancer or propensity to develop cancer, monitoring the efficacy of cancer treatment, identifying inhibitors of Pellino 1 and 2, inhibiting the

CC expression and/or activity of Pellino 1 and 2 in cancer cells, and
 CC treating cancer or inhibiting proliferation of cancer. The cancer can be
 CC epithelial cancer, such as lung, colon, ovarian, breast, prostate,
 CC kidney, stomach, bladder, or any cancer of the gastrointestinal tract
 XX
 SQ Sequence 22 BP; 4 A; 4 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.39; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTGG 22
 |||||
 Db 1 GATGCTGAAGTCGTCCTCATTTGG 22

RESULT 2
 ABN40168/c
 ID ABN40168 standard; DNA; 60 BP.
 XX
 AC ABN40168;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:12916.
 XX
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200210449-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 20-JUL-2001; 2001WO-IB001903.
 XX
 PR 28-JUL-2000; 2000US-0221607P.
 PR 02-MAY-2001; 2001US-0287724P.
 XX
 PA (COMP-) COMPUGEN INC.
 XX
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX
 DR WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a
 PT genome, useful for detecting tissue-, pathology-, and developmental-
 PT specific genes.
 XX
 PS Example 1; SEQ ID NO 12916; 47pp; English.
 XX
 CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
 CC)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises several
 CC oligonucleotides, each capable of hybridizing selectively to a set of
 CC messenger RNAs transcribed from a given transcription unit of the genome,
 CC which encodes one or more messenger RNA splice variants. The
 CC oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a particular
 CC biological or pathological state, and so allowing the detection of tissue
 CC - and pathology-specific genes such as those genes only expressed in
 CC specific tissue under a specific pathological condition; to detect
 CC developmental specific genes; and to detect RNA transcripts and splice
 CC variants of a transcriptome of a patient suffering from a particular
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
 CC rats, humans and mice, which are used in the exemplification of the

CC present invention. N.B. The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 60 BP; 11 A; 15 C; 15 G; 19 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 60;
 Best Local Similarity 100.0%; Pred. No. 0.44; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTGG 22
 |||||
 Db 60 GATGCTGAAGTCGTCCTCATTTGG 39

RESULT 3
 ABZ18999
 ID ABZ18999 standard; cDNA; 259 BP.
 XX
 AC ABZ18999;
 XX
 DT 23-JAN-2003 (first entry)
 XX
 DE Group III cDNA cancer related clone SEQ ID NO:1425.
 XX
 KW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;
 KW immune response; virology; immunology; microbiology; molecular biology;
 KW recombinant DNA technology; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200278516-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US010421.
 XX
 PR 30-MAR-2001; 2001US-0280255P.
 PR 28-AUG-2001; 2001US-0315563P.
 PR 09-JAN-2002; 2002US-0347313P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Wang T, Wang S, Bangur CS, Gaiger A;
 XX
 DR WPI; 2003-058387/05.

XX New immunogenic polynucleotides or polypeptides useful for diagnosing,
 PT preventing and treating cancer expressing CT or CP mRNA antigens, and in
 PT virology, immunology, microbiology, molecular biology and recombinant DNA
 PT techniques.
 XX
 PS Claim 1; SEQ ID NO 1425; 207pp; English.
 XX
 CC ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and
 CC ABP54446 to ABP54472 represent protein (II) sequences, from the present
 CC invention. (I) and (II) have cytostatic activity and can be used in gene
 CC therapy and vaccines. (I), (II), antibodies and compositions from the
 CC present invention are useful for diagnosing, preventing and treating
 CC cancer, which expresses CT or CP mRNA antigens. They are useful for
 CC stimulating immune response. They can also be useful in virology,
 CC immunology, microbiology, molecular biology and recombinant DNA
 CC techniques. N.B. The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 259 BP; 89 A; 50 C; 59 G; 61 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 259;
 Best Local Similarity 100.0%; Pred. No. 0.54; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTGG 22

XX OS Homo sapiens.
 XX PN WO200155320-A2.
 XX XX
 PD 02-AUG-2001.
 XX XX
 PF 17-JAN-2001; 2001WO-US001339.
 XX XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226379P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226688P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 06-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 21-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 25-SEP-2000; 2000US-0234999P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-02559679P.
 XX XX

PA (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-465570/50.
 XX Isolated nucleic acid molecule encoding a reproductive system antigen is
 PT used in preventing, treating or ameliorating a medical condition.
 PT Disclosure; SEQ ID NO 7043; 1297pp + Sequence Listing; English.
 XX The present invention provides the protein and coding sequences of a
 CC number of human reproductive system related antigens. These can be used
 CC in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a genomic sequence encoding a
 CC protein of the invention
 XX Sequence 3614 BP; 1063 A; 621 C; 657 G; 1273 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 22; DB 4; Length 3614;
 Best Local Similarity 100.0%; Pred. No. 0.76;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GATGCTGAAGTCTCTCATGG 22
 DB 3085 GATGCTGAAGTCTCTCATGG 3064
 RESULT 7
 AAL04354/c
 ID AAL04354 standard; DNA; 3615 BP.
 XX AAL04354;
 AC AAL04354;
 DT 21-NOV-2001 (first entry)
 XX Human reproductive system related antigen DNA SEQ ID NO: 7042.
 XX Human; reproductive system related antigen; reproductive system disorder;
 KW cancer; gene therapy; ds.
 KW Homo sapiens.
 OS WO200155320-A2.
 PN 02-AUG-2001.
 PD 17-JAN-2001; 2001WO-US001339.
 PF 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 11-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 14-JUL-2000; 2000US-0217496P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226686P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.

PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234224P.
 PR 25-SEP-2000; 2000US-0234937P.
 PR 25-SEP-2000; 2000US-0234938P.
 PR 26-SEP-2000; 2000US-0234984P.
 PR 27-SEP-2000; 2000US-0234985P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.

PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM,
 PI
 XX WPI; 2001-465570/50.
 XX
 XX Isolated nucleic acid molecule encoding a reproductive system antigen is
 PT used in preventing, treating or ameliorating a medical condition.
 XX
 XX Disclosure; SEQ ID NO 7041; 1297pp + Sequence Listing; English.
 XX
 XX The present invention provides the protein and coding sequences of a
 CC number of human reproductive system related antigens. These can be used
 CC in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a genomic sequence encoding a
 CC protein of the invention
 XX
 XX Sequence 3752 BP; 1101 A; 648 C; 671 G; 1332 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 22; DB 4; Length 3752;
 Best Local Similarity 100.0%; Pred. NO. 0.76;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GATGCTGAAGTGTCTTCATTGG 22
 |||||
 DB 3086 GATGCTGAAGTGTCTTCATTGG 3065
 RESULT 9
 ACC42349/C
 ID ACC42349 standard; cDNA; 5579 BP.
 XX
 AC ACC42349;
 XX
 DT 22-MAY-2003 (first entry)
 XX
 XX Human MAP kinase cascade activator #59 cDNA.
 XX
 KW Human; Elki phosphorylation; Elki phosphorylation kinase; virucide;
 KW antinflammatory; immunomodulator; cytostatic; antiallergic; anti-HIV;
 KW antirheumatic; antiarthritic; antidiabetic; antidiabetic; gene therapy;
 KW inflammation; autoimmune disease; viral disease; cancer; diabetes;
 KW rheumatoid arthritis; asthma; allergic rhinitis; AIDS; viral hepatitis;
 KW Iga nephritis; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO2003008589-A1.
 XX
 XX 30-JAN-2003.
 XX
 XX 15-JUL-2002; 2002WO-JP007174.
 XX
 XX 18-JUL-2001; 2001JP-00218204.
 XX
 XX 31-AUG-2001; 2001JP-00263450.
 XX
 XX 21-JAN-2002; 2002JP-00012176.
 XX
 XX (ASAH) ASAH KASEI KOGYO KK.
 PA
 XX Matsuzaki O, Matsuda A, Nagano Y, Suzuki N;
 PI
 XX WPI; 2003-229582/22.
 DR
 XX P-PSDB; ABR41083.
 PT
 Elki phosphorylation-associated gene and its encoded protein with MAP
 kinase cascade effect, applicable in diagnosis of and developing drugs

PT for e.g. inflammations, autoimmune diseases, viral diseases and cancer.
XX
XX
XX Claim 4; Page 631-640; 762pp; Japanese.
XX
XX The invention relates to a novel purified protein having Elkl
CC phosphorylation activity and/or an activity of activating Elkl
CC phosphorylation kinase. A protein of the invention has antiinflammatory,
CC immunomodulator, virucide, cytostatic, antiallergic, antirheumatic,
CC antiarthritic, antidiabetic, antisthmatic, and anti-HIV activity. The
CC polynucleotides may have a use in gene therapy. The gene and its encoded
CC protein are applicable in diagnosis of and developing drugs for e.g.
CC inflammations, autoimmune diseases, viral diseases and cancer such as
CC rheumatoid arthritis, diabetes; asthma, allergic rhinitis, AIDS, viral
CC hepatitis and lga nephritis. The present sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 5579 BP; 1535 A; 1111 C; 1214 G; 1719 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 8; Length 5579;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GATGCTGAAGTCGTCCTCATGG 22
Db 5135 GATGCTGAAGTCGTCCTCATGG 5114
RESULT 10
ABA95158/c
ID ABA95158 standard; DNA; 2182 BP.
XX
AC ABA95158;
XX
XX 07-AUG-2003 (revised)
DT 20-MAY-2002 (first entry)
XX
DE S. castellii glucoamylase (GAM) promoter sequence.
XX
XX Yeast; glucoamylase; GAM gene; gene expression; transcription; promoter;
KW ds.
XX
XX Debaryomyces sp.
XX
XX
FH Key Location/Qualifiers
FT TATA_signal 1561..1565 /*tag= a
FT CAAT_signal 1571..1574 /*tag= b
FT TATA_signal 1626..1643 /*tag= c
FT CAAT_signal 1709..1712 /*tag= d
FT TATA_signal 1730..1734 /*tag= e
FT CAAT_signal 1776..1779 /*tag= f
FT CAAT_signal 1805..1808 /*tag= g
FT CAAT_signal 1816..1819 /*tag= h
FT TATA_signal 1864..1868 /*tag= i
FT TATA_signal 1884..1887 /*tag= j
FT TATA_signal 1937..1943 /*tag= k
FT CAAT_signal 1963..1966 /*tag= l
FT CAAT_signal 2015..2018 /*tag= m
FT TATA_signal 2034..2037 /*tag= n
FT TATA_signal 2039..2043

FT TATA_signal /*tag= o
FT 2081..2090 /*tag= p
FT TATA_signal 2135..2139 /*tag= q
FT misc_feature 2148..2150 /*tag= r
FT /note= "start codon"
XX
PN WO200212516-A2.
XX
PD 14-FEB-2002.
XX
XX 03-AUG-2001; 2001WO-US024476.
XX
XX 04-AUG-2000; 2000US-00632314.
XX
XX 02-AUG-2001; 2001US-00921944.
XX
XX (BATT) BATTELLE MEMORIAL INST.
XX
XX Gao J, Skeen RS, Hooker BS, Anderson DB;
XX
XX WPI; 2002-227159/28.
XX
XX Novel isolated yeast promoter native to Schwannomyces castellii and
PT located upstream of and in control of glucoamylase gene, useful for
PT expressing gene of interest in bacterial, yeast, mold, plant/plant cell
PT species.
XX
XX Example 2; Fig 4; 28pp; English.
XX
XX The invention provides an isolated yeast promoter, which is native to
CC Schwannomyces castellii (ATCC 26077) and located upstream of and in
CC control of a glucoamylase (GAM) gene. The GAM promoter or a vector
CC comprising the promoter is useful for expressing a gene of interest in
CC bacterial, yeast, mold and plant/plant cell species. The GAM promoter is
CC useful for regulating strong gene expression in starch culture medium,
CC for directing transcription or expression of a gene of interest, for
CC regulating native or foreign gene expression in native or heterologous
CC host strains with starch, and for certain types of metabolic pathway
CC controlling and foreign pathway accumulation. The present sequence
CC represents the S. castellii GAM promoter sequence. (Updated on 07-AUG-
XX 2003 to correct OS field.)
XX
SQ Sequence 2182 BP; 713 A; 355 C; 343 G; 771 T; 0 U; 0 Other;
Query Match 78.2%; Score 17.2; DB 6; Length 2182;
Best Local Similarity 86.4%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GATGCTGAAGTCGTCCTCATGG 22
Db 103 GAGGCTGAAGTCGTCGATGG 82
RESULT 11
ACA45178/c
ID ACA45178 standard; DNA; 2415 BP.
XX
XX
AC ACA45178;
XX
XX 19-JUN-2003 (first entry)
XX
XX Prokaryotic essential gene #26835.
XX
XX Antisense; ds; prokaryotic essential gene; cell proliferation;
XX drug design; gene.
XX
XX Pseudomonas syringae.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US0009107.
XX
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haseelbeck R, Ohlsen KL, Zyskind JW,
PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR P-PSDB; ABU41308.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 14; SEQ ID NO 33048; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pat_sequences
XX
XX Sequence 2415 BP; 605 A; 699 C; 658 G; 453 T; 0 U; 0 Other;
SQ
Query Match 78.2%; Score 17.2; DB 8; Length 2415;
Best Local Similarity 86.4%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GATGCTGAAGTCGTCCTCATGG 22
|||||
Db 189 GATGCTGAAGTCGTCGTCATGG 168
RESULT 12
ABX77573
ID ABX77573 standard; cDNA; 3634 BP.
XX
AC ABX77573;
XX
DT 09-APR-2003 (first entry)

XX Differentially expressed breast cancer associated cDNA #68.
DE
XX Breast cancer; differential gene expression; BC-cDNA;
KW breast cancer diagnosis; breast cancer monitoring;
KW breast cancer treatment; breast cancer staging; gene, ss.
XX
OS Homo sapiens.
XX
XX US2002156263-A1.
PN
XX 24-OCT-2002.
PD
XX 04-OCT-2001; 2001US-00974298.
PF
XX 05-OCT-2000; 2000US-0238331P.
PR
XX (CHEN/) CHEN H.
PA
XX Chen H;
PI
XX WPI; 2003-182653/18.
DR
XX New cDNAs, which are differentially expressed in (metastatic) breast
PT cancer useful for diagnosing or staging, breast cancer, or for monitoring
PT the treatment of breast cancer in an individual.
XX
XX Claim 1; SEQ ID NO 83; 30pp; English.
PS
XX The invention describes a combination of cDNAs (designated BC-cDNAs),
CC which are differentially expressed in breast cancer. The combination
CC includes 152 cDNA sequences, or their complements. The protein encoded by
CC any of these BC-cDNAs is useful for screening several molecules or
CC compounds to identify at least one ligand that specifically binds the
CC protein, producing or preparing polyclonal or monoclonal antibodies, or
CC purifying antibodies from a sample. The antibodies, which specifically
CC bind the protein differentially expressed in breast cancer is useful for
CC detecting the expression of a protein in a sample. The BC-cDNAs are also
CC useful for diagnosing, monitoring the treatment of, or staging, breast
CC cancer. This sequence represents a differentially expressed breast cancer
CC associated cDNA. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=20020156263
XX
XX Sequence 3634 BP; 992 A; 928 G; 932 G; 781 T; 0 U; 1 Other;
SQ
Query Match 78.2%; Score 17.2; DB 8; Length 3634;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GATGCTGAAGTCGTCCTCATGG 22
|||||
Db 805 GATGCTGAAGTCCTCACAGTGG 826
RESULT 13
ABQ92052
ID ABQ92052 standard; cDNA; 4070 BP.
XX
AC ABQ92052;
XX
XX 04-OCT-2002 (first entry)
DT
XX Human polynucleotide SEQ ID NO 49.
DE
XX Human; cytostatic; antirheumatic; antiarthritic; vulnery; analgesic;
KW antinflammatory; antibacterial; immunosuppressive; antiparkinsonian;
KW neuroprotective; nootropic; osteopathic; haemostatic; vasotropic;
KW antiulcer; fungicide; antidiabetic; antisthmatic; antiallergic;
KW immunostimulant; antiparasitic; secreted protein; transmembrane protein;
KW cytokine; cell proliferation; cell differentiation; autoimmune disease;
KW stem cell; growth factor; nervous system disease; neuropathy;

KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
 KW osteoporosis; severe combined immunodeficiency; SCID; infection;
 KW multiple sclerosis; rheumatoid arthritis; gene therapy; gene; ss.
 XX Homo sapiens.
 OS US2002065394-A1.
 PN 30-MAY-2002.
 PD 22-DEC-2000; 2000US-00745763.
 XX 18-MAR-1998; 98US-00040963.
 XX (JACO/) JACOBS K.
 PA (MCCO/) MCCOY J M.
 PA (LAVA/) LAVALLIE E R.
 PA (COLL/) COLLINS-RACIE L A.
 PA (EVAN/) EVANS C.
 PA (MERB/) MERBERG D.
 PA (TREA/) TREACY M.
 PA (SPAU/) SPAULDING V.
 XX Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Spaulding V;
 XX WPI; 2002-582343/62.
 DR P-PSDB; ABP61838.
 XX Novel secreted or transmembrane protein and polynucleotide encoding the
 PT protein, useful for diagnosis and treatment of neurological disorders,
 PT cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.
 XX Claim 174; Page 182-183; 284pp; English.
 XX The invention relates to human secreted or transmembrane protein (I),
 CC their fragments and is encoded by specific complementary deoxyribonucleic
 CC acid (cDNA) inserts (II), where the protein is substantially free from
 CC other mammalian proteins. (I) are useful for preventing, treating or
 CC ameliorating a medical condition, especially immunological treatment or
 CC prevention of tumours. (I) exhibits activity relating to angiogenesis,
 CC cytokine, cell proliferation, cell differentiation, antiinflammatory,
 CC stem cell growth factor activity and activin or inhibin-related
 CC activities (I) can be used to manipulate stem cells in culture to give
 CC rise to neuroepithelial cells that can be used to augment or replace
 CC cells damaged by illness, autoimmune disease, accidental damage or
 CC genetic disorders. (I) induces the proliferation of neural cells and
 CC regeneration of nerve and brain tissue and is useful for the treatment of
 CC central and peripheral nervous system diseases and neuropathies, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis. (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopaenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth and in tissue repair, healing of burns, incisions, ulcers,
 CC for treating osteoporosis, osteoarthritis, bone degenerative disorders or
 CC periodontal disease. (I) is also useful for gut protection or
 CC regeneration and treatment of lung or liver fibrosis, reperfusion injury
 CC in various tissues, various immune deficiencies and disorders including
 CC severe combined immunodeficiency (SCID), bacterial or fungal infections,
 CC autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis,
 CC diabetes mellitus, myasthenia gravis, allergic reactions and conditions,
 CC such as asthma or other respiratory problems. (II) is useful to express
 CC recombinant protein, as markers for tissues in which the corresponding
 CC protein is preferentially expressed and in gene therapy. The present
 CC sequence is that of a polynucleotide of the invention
 XX Sequence 4070 BP; 1098 A; 1034 C; 1012 G; 921 T; 0 U; 5 Other;
 SQ Query Match 78.2%; Score 17.2; DB 6; Length 4070;
 Best Local Similarity 86.4%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTCATTCG 22
 DB 1357 GATGCTGAAGTCCTCACAGTCG 1378
 RESULT 14
 AAV62749
 ID AAV62749 standard; cDNA; 4130 BP.
 XX AAV62749;
 XX 15-FEB-1999 (first entry)
 XX Human secreted protein clone er418_5 cDNA.
 DE Secreted protein; human; er418_5; ds.
 KW Homo sapiens.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 571..3306
 FT /*tag= a
 XX WO9846757-A2.
 PN 22-OCT-1998.
 PD 14-APR-1998; 98WO-0007999.
 XX 15-APR-1997; 97US-00843374.
 PR 13-APR-1998; 98US-00059487.
 XX (GEWY) GENETICS INST INC.
 XX Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
 PI Spaulding V, Agostino MJ;
 XX WPI, 1998-568731/48.
 DR P-PSDB; AAW74723.
 XX New polynucleotide(s) encoding secreted human proteins - are derived
 PT from, e.g. human foetal brain or foetal kidney cDNA libraries,
 PT potentially useful as, e.g. vaccines or thrombolytic agents.
 XX Claim 19; Page 76-78; 120pp; English.
 XX Full-length cDNA clone er418_5 includes an open reading frame encoding a
 CC human secreted protein (see AAW74723). It was isolated from a human
 CC foetal brain cDNA library using methods which are selective for cDNAs
 CC encoding secreted proteins, or was identified as encoding a secreted or
 CC transmembrane protein on the basis of computer analysis of the amino acid
 CC sequence of the encoded protein. It shows some similarity to database
 CC sequences. The invention provides polynucleotides (see AAV62746-55) from
 CC human foetal brain, adult testis, adult brain, adult kidney and foetal
 CC kidney (all deposited as composite clone ATCC 98404), which encode human
 CC secreted proteins (see AAW74720-29). The polynucleotides and proteins are
 CC predicted to have biological activities which would make them suitable
 CC for treating, preventing or ameliorating medical conditions in humans and
 CC animals, although no supporting data are given. Suggested activities
 CC include nutritional activity, immune stimulating (e.g. as vaccines) or
 CC suppressing activity, haematopoiesis regulating activity, tissue growth
 CC activity, activin/inhibin activity, chemotactic/chemokinetic activity,
 CC haemostatic and thrombolytic activity, receptor/ligand activity,
 CC antiinflammatory activity, cadherin/tumour invasion suppressor activity,
 CC and tumour inhibition activity. The polynucleotides are also stated to be
 CC useful for gene therapy, and can be used in recombinant production of the
 CC polypeptides
 XX Sequence 4130 BP; 1113 A; 1051 C; 1024 G; 936 T; 0 U; 6 Other;
 SQ Query Match 78.2%; Score 17.2; DB 2; Length 4130;
 Best Local Similarity 86.4%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGCTCTCATTTG 22
 |||||
 Db 1417 GATGCTGAAGTCGCTCTCACAGTGG 1438

RESULT 15

ADQ64976
 ID ADQ64976 standard; cDNA; 4799 BP.
 XX
 AC ADQ64976;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Novel human cDNA sequence #2137.
 XX
 KW ss; gene; osteopathic; neuroprotective; neurotropic; antiparkinsonian;
 KW cytosolic; gene therapy; diagnostic marker; morbid state; osteoporosis;
 KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN EP1440981-A2.
 XX
 PD 28-JUL-2004.
 XX
 PF 21-JAN-2004; 2004EP-00001196.
 XX
 PR 21-JAN-2003; 2003JP-00102206.
 PR 09-MAY-2003; 2003JP-00131392.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Nagai K, Irie R;
 XX
 DR WPI; 2004-535376/52.
 DR P-PSDB; ADQ67164.
 XX
 PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 XX
 PS Claim 1; SEQ ID NO 2137; 2449pp; English.
 XX
 CC The invention relates to 2495 novel polynucleotides (I) and their encoded
 CC polypeptides, sequences hybridizing to these nucleotides, sequences
 CC encoding partial polypeptides and sequences having 70% or 90% identity to
 CC the nucleotide and protein sequences. The nucleotides and polypeptides
 CC are useful as diagnostic markers or therapeutic target for the diseases
 CC or morbid states. They are also useful for treating osteoporosis,
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
 CC dementia and various cancers. This sequence corresponds to a nucleotide
 CC sequence of the invention.
 XX
 SQ Sequence 4799 BP; 1251 A; 1234 C; 1233 G; 1081 T; 0 U; 0 Other;

Query Match 78.2%; Score 17.2; DB 12; Length 4799;
 Best Local Similarity 86.4%; Pred. No. 2.le+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGCTCTCATTTG 22
 |||||
 Db 2101 GATGCTGAAGTCGCTCTCACAGTGG 2122

Search completed: July 20, 2005, 17:31:34
 Job time : 208.348 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 16:53:52 ; Search time 69.3478 Seconds
(without alignments)
519.095 Million cell updates/sec

Title: US-10-041-030-7

Perfect score: 22
Sequence: 1 gatgctgaagtcgtctcattgg 22

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfileseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.2	78.2	579	US-09-248-796A-12736	Sequence 12736, A
2	17.2	78.2	1230025	US-09-198-452A-1	Sequence 1, Appli
3	17.2	78.2	1230230	US-09-438-185A-1	Sequence 1, Appli
4	17	77.3	958	US-09-602-777A-77	Sequence 77, Appli
C 5	16.8	76.4	1830121	US-09-557-88A-1	Sequence 1, Appli
C 6	16.8	76.4	1830121	US-09-643-990A-1	Sequence 1, Appli
C 7	16.4	74.5	601	US-09-949-016-199193	Sequence 199193, A
8	16.4	74.5	98708	US-09-949-016-16392	Sequence 16392, A
9	16.2	73.6	204	US-09-540-236-836	Sequence 836, App
10	16.2	73.6	318	US-09-248-796A-8067	Sequence 8067, Ap
11	16.2	73.6	601	US-09-949-016-187670	Sequence 187670, A
12	16.2	73.6	1001	US-09-671-317-42	Sequence 42, Appli
C 13	16.2	73.6	6553	US-09-799-451-581	Sequence 581, App
14	16.2	73.6	49617	US-09-596-002-28	Sequence 28, Appli
15	16.2	73.6	66085	US-09-949-016-13292	Sequence 13292, A
C 16	16.2	73.6	96690	US-09-949-016-17103	Sequence 17103, A
17	16.2	73.6	194915	US-09-949-016-15584	Sequence 15584, A
18	16.2	73.6	390890	US-09-949-016-14720	Sequence 14720, A
19	15.8	71.8	601	US-09-949-016-91218	Sequence 91218, A
C 20	15.8	71.8	601	US-09-949-016-163448	Sequence 163448, A
C 21	15.8	71.8	3307	US-09-949-016-1973	Sequence 1973, Ap
C 22	15.8	71.8	3412	US-09-949-016-2202	Sequence 2202, Ap
C 23	15.8	71.8	3415	US-09-949-016-693	Sequence 693, App
C 24	15.8	71.8	3418	US-09-193-562B-29	Sequence 29, Appli
C 25	15.8	71.8	3418	US-10-055-412B-29	Sequence 29, Appli
C 26	15.8	71.8	25111	US-09-949-016-12435	Sequence 12435, A
C 27	15.8	71.8	25111	US-09-949-016-13944	Sequence 13944, A

28	15.8	71.8	85869	4	US-09-949-016-12017	Sequence 12017, A
29	15.8	71.8	85878	4	US-09-949-016-16321	Sequence 16321, A
30	15.8	71.8	110266	4	US-09-949-016-14913	Sequence 14913, A
31	15.8	71.8	110266	4	US-09-949-016-14914	Sequence 14914, A
32	15.8	71.8	110266	4	US-09-949-016-14915	Sequence 14915, A
33	15.8	71.8	110266	4	US-09-949-016-14916	Sequence 14916, A
34	15.8	71.8	110266	4	US-09-949-016-14917	Sequence 14917, A
35	15.8	71.8	110266	4	US-09-949-016-14918	Sequence 14918, A
36	15.8	71.8	110266	4	US-09-949-016-14919	Sequence 14919, A
37	15.8	71.8	110266	4	US-09-949-016-14920	Sequence 14920, A
38	15.8	71.8	110266	4	US-09-949-016-14921	Sequence 14921, A
39	15.8	71.8	110266	4	US-09-949-016-14922	Sequence 14922, A
C 40	15.8	71.8	125902	4	US-09-949-016-13715	Sequence 13715, A
41	15.8	71.8	175236	4	US-09-949-016-14353	Sequence 14353, A
C 42	15.6	70.9	287	1	US-09-985-799-70	Sequence 70, Appli
C 43	15.6	70.9	287	1	US-09-977-371-70	Sequence 70, Appli
C 44	15.6	70.9	287	1	US-08-594-031-70	Sequence 70, Appli
C 45	15.6	70.9	413	4	US-09-733-685-22	Sequence 22, Appli

ALIGNMENTS

RESULT 1
US-09-248-796A-12736
; Sequence 12736, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 12736
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-12736

Query Match 78.2%; Score 17.2; DB 4; Length 579;
Best Local Similarity 86.4%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GATGCTGAAGTCGTCTCATTGG 22
DB 511 GTTGCTGAAGCCTTCTCATTGG 532

RESULT 2
US-09-198-452A-1
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc_feature

```
LOCATION: (1)..(15000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (15001)..(30000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (30001)..(45000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (45001)..(60000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (60001)..(75000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (75001)..(90000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (90001)..(105000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (105001)..(120000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (120001)..(135000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (135001)..(150000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (150001)..(165000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (165001)..(180000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (180001)..(195000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (195001)..(210000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (210001)..(225000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (225001)..(240000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (240001)..(255000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (255001)..(270000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (270001)..(285000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (285001)..(300000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (300001)..(315000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (315001)..(330000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (330001)..(345000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (345001)..(360000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (360001)..(375000)
```



```
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 77
; LENGTH: 958
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(958)
; OTHER INFORMATION: RXA01151
US-09-602-777A-77

Query Match          77.3%; Score 17; DB 4; Length 958;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTC 17
    |||||
Db 241 GATGCTGAAGTCGTCCTC 257

RESULT 5
US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; FILING DATE: JUN-5-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB186P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Query Match          76.4%; Score 16.8; DB 4; Length 1830121;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATGCTGAAGTCGTCCTCATG 21
    |||||
Db 1553535 ATGCTGAAGTCGTCCTCATG 1553516

RESULT 6
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
; APPLICANT: Robert D. Fleischmann
; Mark D. Adams
; Owen White
; Hamilton O. Smith
; J. Craig Venter
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville,
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,990A
; FILING DATE: 23-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,429
; FILING DATE: 1995-06-07
; APPLICATION NUMBER: 08/426,787
; FILING DATE: 1995-04-21
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB186P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5790
; TELEFAX: 310-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Query Match          76.4%; Score 16.8; DB 4; Length 1830121;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATGCTGAAGTCGTCCTCATG 21
    |||||
Db 1553535 ATGCTGAAGTCGTCCTCATG 1553516

RESULT 7
US-09-949-016-199193/c
; Sequence 199193, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
```


; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199193
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-199193

Query Match 74.5%; Score 16.4; DB 4; Length 601;
Best Local Similarity 85.0%; Pred. No. 97;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGCTGAAGTCGTCCTCATGG 22
||:|||||
Db 303 TGSTGAGGTCCTCTCATGG 284

RESULT 8

US-09-949-016-16392
; Sequence 16392, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16392
; LENGTH: 98708
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(98708)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16392

Query Match 74.5%; Score 16.4; DB 4; Length 98708;
Best Local Similarity 94.4%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATGCTGAAGTCGTCCTCAT 19
|||||
Db 5315 ATGCTGAAGTCGTCCTCAT 5332

RESULT 9

US-09-540-236-836
; Sequence 836, Application US/09540236
; Patent No. 6673910

GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; NUMBER OF SEQ ID NOS: 3840

; SEQ ID NO 836
; LENGTH: 204
; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-836

Query Match 73.6%; Score 16.2; DB 4; Length 204;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTCAT 21
||:|||||
Db 172 GAAGCTGAAGTCGCCCAT 192

RESULT 10

US-09-248-796A-8067
; Sequence 8067, Application US/09248796A
; Patent No. 6747137

GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 8067
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-8067

Query Match 73.6%; Score 16.2; DB 4; Length 318;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGCTGAAGTCGTCCTCAT 22
||:|||||
Db 17 ACGCTGAAGTCGCTCAT 37

RESULT 11

US-09-949-016-187670
; Sequence 187670, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187670
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-187670

Query Match 73.6%; Score 16.2; DB 4; Length 601;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGCTGAAGTCGTCTCATTTGG 22
 ||||| ||||| ||||| |||||
 Db 164 ATGCTGAAGTCGTCTCATTTGG 184

RESULT 12
 US-09-671-317-42
 ; Sequence 42, Application US/09671317
 ; Patent No. 6528260
 ; GENERAL INFORMATION:
 ; APPLICANT: Blumenfeld, Marta
 ; APPLICANT: Chumakov, Ilya
 ; APPLICANT: Bougueleret, Lydie
 ; APPLICANT: Cohen, Annick
 ; TITLE OF INVENTION: BIOMOLECULAR MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
 ; FILE REFERENCE: 62 US3.CIP
 ; CURRENT APPLICATION NUMBER: US/09/671,317
 ; CURRENT FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US 09/536,178
 ; PRIOR FILING DATE: 2000-03-23
 ; PRIOR APPLICATION NUMBER: PCT/IB00/00403
 ; PRIOR FILING DATE: 2000-03-24
 ; PRIOR APPLICATION NUMBER: US 60/126,269
 ; PRIOR FILING DATE: 1999-03-25
 ; PRIOR APPLICATION NUMBER: US 60/131,961
 ; PRIOR FILING DATE: 1999-04-30
 ; NUMBER OF SEQ ID NOS: 977
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 42
 ; LENGTH: 1001
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 503
 ; OTHER INFORMATION: 12-723-293 : polymorphic base C or T
 ; NAME/KEY: misc_binding
 ; LOCATION: 484..502
 ; OTHER INFORMATION: 12-723-293.mis1
 ; NAME/KEY: misc_binding
 ; LOCATION: 504..523
 ; OTHER INFORMATION: 12-723-293.mis2, potential complement
 ; NAME/KEY: primer_bind
 ; LOCATION: 210..230
 ; OTHER INFORMATION: upstream amplification primer
 ; NAME/KEY: primer_bind
 ; LOCATION: 591..610
 ; OTHER INFORMATION: downstream amplification primer, complement
 ; NAME/KEY: misc_binding
 ; LOCATION: 491..515
 ; OTHER INFORMATION: 12-723-293 potential probe
 ; NAME/KEY: misc_feature
 ; LOCATION: 312..379
 ; OTHER INFORMATION: n=a, g, c or t
 ; US-09-671-317-42

Query Match 73.6%; Score 16.2; DB 4; Length 1001;
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGCTGAAGTCGTCTCATTTGG 22
 ||||| ||||| ||||| |||||
 Db 551 ATGTTGATGCTCTTCATTTGG 571

RESULT 13
 US-09-799-451-581/c
 ; Sequence 581, Application US/09799451
 ; Patent No. 6783969
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping
 ; APPLICANT: Goodrich, Ryle
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Ma, Yungqing
 ; APPLICANT: Yamazaki, Victoria
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Ghosh, Reena
 ; APPLICANT: Dmanac, Radoje T.
 ; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
 ; FILE REFERENCE: Polypeptides
 ; CURRENT APPLICATION NUMBER: US/09/799,451
 ; CURRENT FILING DATE: 2001-03-05
 ; NUMBER OF SEQ ID NOS: 948
 ; SOFTWARE: pt_FL_genes Version 2.0
 ; SEQ ID NO 581
 ; LENGTH: 6553
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (272)..(5242)
 ; US-09-799-451-581

Query Match 73.6%; Score 16.2; DB 4; Length 6553;
 Best Local Similarity 85.7%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGCTGAAGTCGTCTCATTTGG 22
 ||||| ||||| ||||| |||||
 Db 2809 ATTATGAAGTCGTCTCATTTGG 2789

RESULT 14
 US-09-596-002-28
 ; Sequence 28, Application US/09596002
 ; Patent No. 6632836
 ; GENERAL INFORMATION:
 ; APPLICANT: Lagace, Robert, E.
 ; APPLICANT: Patterson, Chandra
 ; APPLICANT: Berg, Kim, L.
 ; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
 ; FILE REFERENCE: PM-0008-4 US
 ; CURRENT APPLICATION NUMBER: US/09/596,002
 ; CURRENT FILING DATE: 2000-06-16
 ; PRIOR APPLICATION NUMBER: 60/140,121
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 28
 ; LENGTH: 49617
 ; TYPE: DNA
 ; ORGANISM: M. catarrhalis
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: incyte template ID No. 6632636 28
 ; PUBLICATION INFORMATION:
 ; US-09-596-002-28

Query Match 73.6%; Score 16.2; DB 4; Length 49617;
 Best Local Similarity 85.7%; Pred. No. 3e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCTCATTTG 21

Db 22308 GAAGCTGAAGTCGCCACATTG 22328

RESULT 15

```

US-09-949-016-13292
; Sequence 13292, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE OF INVENTION: CU001307
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13292
; LENGTH: 66065
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(66065)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13292

```

Query Match 73.6%; Score 16.2; DB 4; Length 66065;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCTCATTTG 21
|||
Db 63263 GATGCTGATGTCCTCTTATTG 63283

Search completed: July 20, 2005, 18:58:55
Job time : 79.3478 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 18:01:31 ; Search time 308.957 Seconds
(without alignments)
451.758 Million cell updates/sec

Title: US-10-041-030-7
Perfect score: 22
Sequence: 1 gatcgtgaagtcgtctcattgg 22

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues

Total number of hits satisfying chosen parameters: 14346486

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications, NA: *

1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10:	/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12:	/cgn2_6/ptodata/2/pubpna/US09D_PUBCOMB.seq.*
13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14:	/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16:	/cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17:	/cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18:	/cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
19:	/cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
20:	/cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
21:	/cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
22:	/cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq.*
23:	/cgn2_6/ptodata/2/pubpna/US10K_PUBCOMB.seq.*
24:	/cgn2_6/ptodata/2/pubpna/US10L_PUBCOMB.seq.*
25:	/cgn2_6/ptodata/2/pubpna/US10M_PUBCOMB.seq.*
26:	/cgn2_6/ptodata/2/pubpna/US10N_PUBCOMB.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	60	13	US-10-041-030-7
2	22	100.0	22	10	US-09-908-975-12916
3	22	100.0	864	15	US-10-106-698-1323
4	22	100.0	3614	10	US-09-764-891-7043
5	22	100.0	3615	10	US-09-764-891-7042
6	22	100.0	3752	10	US-09-764-891-7041
7	22	100.0	5579	14	US-10-197-666A-135

Sequence 287, App	17	US-10-085-117-287	5597	100.0	22	100.0	5597	17	US-10-085-117-287	Sequence 287, App
Sequence 3, Appli	13	US-10-041-030-3	5921	100.0	22	100.0	5921	13	US-10-041-030-3	Sequence 3, Appli
Sequence 286, App	17	US-10-085-117-286	202802	100.0	22	100.0	202802	17	US-10-085-117-286	Sequence 286, App
Sequence 81792, A	20	US-10-425-115-81792	498	79.1	17.4	79.1	498	20	US-10-425-115-81792	Sequence 81792, A
Sequence 46999, A	13	US-10-027-632-46999	593	79.1	17.4	79.1	593	13	US-10-027-632-46999	Sequence 46999, A
Sequence 97451, A	17	US-10-027-632-97451	593	79.1	17.4	79.1	593	17	US-10-027-632-97451	Sequence 97451, A
Sequence 8, Appli	18	US-10-424-599-8	1154	78.2	17.2	78.2	1154	18	US-10-424-599-8	Sequence 8, Appli
Sequence 33048, A	9	US-09-921-9448-8	2182	78.2	17.2	78.2	2182	9	US-09-921-9448-8	Sequence 33048, A
Sequence 93, Appli	17	US-10-282-122A-33048	2415	78.2	17.2	78.2	2415	17	US-10-282-122A-33048	Sequence 93, Appli
Sequence 139, App	9	US-09-974-298-83	3634	78.2	17.2	78.2	3634	9	US-09-974-298-83	Sequence 139, App
Sequence 1, Appli	17	US-10-289-762-1	4130	78.2	17.2	78.2	4130	17	US-10-289-762-1	Sequence 1, Appli
Sequence 1654, Ap	17	US-09-738-626-1654	1581	77.3	17.2	77.3	1581	17	US-09-738-626-1654	Sequence 1654, Ap
Sequence 17676, A	20	US-10-719-993-6815	1980090	77.3	17.2	77.3	1980090	20	US-10-719-993-6815	Sequence 17676, A
Sequence 1, Appli	21	US-10-741-600-17676	3309400	77.3	17.2	77.3	3309400	21	US-10-741-600-17676	Sequence 1, Appli
Sequence 22345, A	9	US-09-738-626-1	1770	76.4	16.8	76.4	1770	9	US-09-738-626-1	Sequence 22345, A
Sequence 8055, Ap	17	US-10-282-122A-22345	2065	76.4	16.8	76.4	2065	17	US-10-282-122A-22345	Sequence 8055, Ap
Sequence 22327, A	18	US-10-425-114-8055	2097	76.4	16.8	76.4	2097	18	US-10-425-114-8055	Sequence 22327, A
Sequence 79, Appli	11	US-09-997-722-79	24080	76.4	16.8	76.4	24080	11	US-09-997-722-79	Sequence 79, Appli
Sequence 1, Appli	17	US-10-329-670-1	1830121	76.4	16.8	76.4	1830121	17	US-10-329-670-1	Sequence 1, Appli
Sequence 1, Appli	20	US-10-158-865-1	1830121	76.4	16.8	76.4	1830121	20	US-10-158-865-1	Sequence 1, Appli
Sequence 5793, Ap	22	US-10-981-687-1	639	74.5	31	16.4	639	22	US-10-981-687-1	Sequence 5793, Ap
Sequence 5794, Ap	13	US-10-027-632-5793	639	74.5	31	16.4	639	13	US-10-027-632-5793	Sequence 5794, Ap
Sequence 5793, Ap	17	US-10-027-632-5793	639	74.5	31	16.4	639	17	US-10-027-632-5793	Sequence 5793, Ap
Sequence 5794, Ap	17	US-10-027-632-5794	639	74.5	31	16.4	639	17	US-10-027-632-5794	Sequence 5794, Ap
Sequence 57780, A	13	US-10-027-632-57780	648	74.5	31	16.4	648	13	US-10-027-632-57780	Sequence 57780, A
Sequence 57781, A	13	US-10-027-632-57781	648	74.5	31	16.4	648	13	US-10-027-632-57781	Sequence 57781, A
Sequence 67920, A	17	US-10-027-632-67920	648	74.5	31	16.4	648	17	US-10-027-632-67920	Sequence 67920, A
Sequence 131822, A	18	US-10-424-599-131822	1126	74.5	40	16.4	1126	18	US-10-424-599-131822	Sequence 131822, A
Sequence 1045, Ap	13	US-10-087-192-1045	24902	74.5	40	16.4	24902	13	US-10-087-192-1045	Sequence 1045, Ap
Sequence 21598, A	9	US-09-864-761-21598	160	73.6	43	16.2	160	9	US-09-864-761-21598	Sequence 21598, A
Sequence 29593, A	18	US-10-424-599-29593	245	73.6	43	16.2	245	18	US-10-424-599-29593	Sequence 29593, A
Sequence 4446, Ap	9	US-09-783-590-4446	454	73.6	45	16.2	454	9	US-09-783-590-4446	Sequence 4446, Ap

ALIGNMENTS

RESULT 1
US-10-041-030-7
Sequence 7, Application US/10041030
Publication No. US20020150934A1
GENERAL INFORMATION:
APPLICANT: Powers, Scott
APPLICANT: Mu, David
APPLICANT: Xiang, Phil
APPLICANT: Peng, Yue
TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Mammalian
TITLE OF INVENTION: Pellino Polypeptides and Polynucleotides
FILE REFERENCE: 018781-006810US
CURRENT APPLICATION NUMBER: US/10/041,030
PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 60/259,502
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
OTHER INFORMATION: probe N63226QF to pellino 2' untranslated region
US-10-041-030-7

Query Match 100.0%; Score 22; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. NO. 0.67;

```
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTGG 22
    |||||
Db 1 GATGCTGAAGTCGTCCTCATTTGG 22

RESULT 2
US-09-908-975-12916/c
; Sequence 12916, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12916
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-12916

Query Match 100.0%; Score 22; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTGG 22
    |||||
Db 60 GATGCTGAAGTCGTCCTCATTTGG 39

RESULT 3
US-10-106-698-1323/c
; Sequence 1323, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1323
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (815)..(815)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (848)..(848)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
```

```
; LOCATION: (862)..(862)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-1323

Query Match 100.0%; Score 22; DB 15; Length 864;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTGG 22
    |||||
Db 333 GATGCTGAAGTCGTCCTCATTTGG 312

RESULT 4
US-09-764-891-7043/c
; Sequence 7043, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7043
; LENGTH: 3614
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7043

Query Match 100.0%; Score 22; DB 10; Length 3614;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTGG 22
    |||||
Db 3085 GATGCTGAAGTCGTCCTCATTTGG 3064

RESULT 5
US-09-764-891-7042/c
; Sequence 7042, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7042
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7042

Query Match 100.0%; Score 22; DB 10; Length 3615;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTGG 22
    |||||
Db 3086 GATGCTGAAGTCGTCCTCATTTGG 3065

RESULT 6
US-09-764-891-7041/c
; Sequence 7041, Application US/09764891
; Publication No. US20030077808A1
```

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7041
; LENGTH: 3752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7041

Query Match 100.0%; Score 22; DB 10; Length 3752;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTGG 22
|||||
Db 3086 GATGCTGAAGTCGTCCTCATTTGG 3065

RESULT 7
US-10-197-666A-135/c
; Sequence 135, Application US/10197666A
; Publication No. US20030092037A1
; GENERAL INFORMATION:
; APPLICANT: ASAH KASEI KABUSIKI KAISYA
; TITLE OF INVENTION: Elki phosphorylation related gene
; FILE REFERENCE: PH-1548US
; CURRENT APPLICATION NUMBER: US/10/197,666A
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: JP 2001-218204
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: JP 2001-263450
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 2002-012176
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 60/305,884
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/316,304
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 60/350,027
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
; LENGTH: 5579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (177)..(1436)
US-10-197-666A-135

Query Match 100.0%; Score 22; DB 14; Length 5579;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTGG 22
|||||
Db 5135 GATGCTGAAGTCGTCCTCATTTGG 5114

RESULT 8
US-10-085-117-287/c
; Sequence 287, Application US/10085117
; Publication No. US2003023234A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.

; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 287
; LENGTH: 5597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-117-287

Query Match 100.0%; Score 22; DB 17; Length 5597;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTGG 22
|||||
Db 5135 GATGCTGAAGTCGTCCTCATTTGG 5114

RESULT 9
US-10-041-030-3/c
; Sequence 3, Application US/10041030
; Publication No. US20020150934A1
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Mu, David
; APPLICANT: Xiang, Phil
; APPLICANT: Peng, Yue
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Mammalian
; FILE REFERENCE: 018781-006810US
; CURRENT APPLICATION NUMBER: US/10/041,030
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/259,502
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 5921
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (501)..(1763)
; OTHER INFORMATION: human pellino 2
US-10-041-030-3

Query Match 100.0%; Score 22; DB 13; Length 5921;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTGG 22
|||||
Db 5459 GATGCTGAAGTCGTCCTCATTTGG 5438

RESULT 10
US-10-085-117-286/c
; Sequence 286, Application US/10085117
; Publication No. US2003023234A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586

```
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 286
; LENGTH: 202802
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-117-286

Query Match      100.0%; Score 22; DB 17; Length 202802;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTCATGG 22
   |||||
Db 192359 GATGCTGAAGTCGTCCTCATGG 192338

RESULT 11
US-10-425-115-81792
; Sequence 81792, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 81792
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_174609C.1
US-10-425-115-81792

Query Match      79.1%; Score 17.4; DB 20; Length 498;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATGCTGAAGTCGTCCTCATTT 20
   |||||
Db 8 ATGTTGAAGTCGTCCTCATTT 26

RESULT 12
US-10-027-632-46999/c
; Sequence 46999, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46999
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-46999

Query Match      79.1%; Score 17.4; DB 17; Length 593;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTCAT 19
   |||||
Db 230 GATGCTGAAGTTGTCTCAT 212

RESULT 13
US-10-027-632-46999/c
; Sequence 46999, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46999
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-46999

Query Match      79.1%; Score 17.4; DB 17; Length 593;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTCAT 19
   |||||
Db 230 GATGCTGAAGTTGTCTCAT 212

RESULT 14
US-10-424-599-97451/c
; Sequence 97451, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
```

```
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46999
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-46999

Query Match      79.1%; Score 17.4; DB 13; Length 593;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTCAT 19
   |||||
Db 230 GATGCTGAAGTTGTCTCAT 212

RESULT 13
US-10-027-632-46999/c
; Sequence 46999, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46999
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-46999

Query Match      79.1%; Score 17.4; DB 17; Length 593;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTCAT 19
   |||||
Db 230 GATGCTGAAGTTGTCTCAT 212

RESULT 14
US-10-424-599-97451/c
; Sequence 97451, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
```



```

; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 97451
; LENGTH: 1154

```

```

1 TYPE: DNA
2 ORGANISM: Glycine max
3 FEATURE:
4 NAME/KEY: (1)..(1154)
5 LOCATION: (1)..(1154)
6 OTHER INFORMATION: unsure at all n locations
7 FEATURE:
8 OTHER INFORMATION: Clone ID: PAT_MRT3847_5901
9 US-0-424-599-97451

```

Query Match 78.2%; Score 17.2; DB 18; Length 1154;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTG 22
|||||
Db 732 GATGCTAAAGTCATCTCACTGG 711

RESULT 15

```

US-09-921-944B-8/c
; Sequence 8, Application US/09921944B
; Patent No. US2002015549A1
; GENERAL INFORMATION:
; APPLICANT: Battelle Memorial Institute
; TITLE OF INVENTION: Isolated Yeast Promoter Sequence and a Method of Regulated Heterod
; TITLE OF INVENTION: Expression
; FILE REFERENCE: E-1823 CIP
; CURRENT APPLICATION NUMBER: US/09/921,944B
; CURRENT FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 2182
; TYPE: DNA
; ORGANISM: Schwanniomyces castellii
US-09-921-944B-8

```

Query Match 78.2%; Score 17.2; DB 9; Length 2182;
Best Local Similarity 86.4%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GATGCTGAAGTCGTCTCATTTG 22 QY
103 GAGGCTGAAGTCGTCTCGATGG 82 db

Search completed: July 20, 2005, 20:42:05
Job time : 318.957 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 15:43:06 ; Search time 1573.48 Seconds
(without alignments)
532.206 Million cell updates/sec

Title: US-10-041-030-7

Perfect score: 22

Sequence: 1 gatgctgaagtcgtctcattgg 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	100.0	403	2	AW386118 RC3-PT000
C 2	22	100.0	451	1	AA905701 OK09206.8
C 3	22	100.0	493	2	AW173368 xj78f06.x
C 4	22	100.0	514	1	AI804454 tc71e02.x
C 5	22	100.0	531	1	AF082809 ox78a02.x
C 6	22	100.0	554	1	AI768516 wh22g11.x
C 7	22	100.0	555	2	BE466421 hz21e08.x
C 8	22	100.0	654	7	CN308828 170006001
C 9	22	100.0	687	5	BQ016066 UI-H-DT1-
C 10	22	100.0	782	5	BQ002692 UI-H-E11-
C 11	22	100.0	895	4	BG283778 602408077
C 12	22	100.0	901	2	BE786617 601478845
C 13	22	100.0	901	4	BG546951 602573943
C 14	22	100.0	943	4	BG388221 602413214
C 15	22	100.0	4308	3	HSMB001459
C 16	20.4	92.7	171	6	CB117270 K-EST0162
C 17	18.8	85.5	645	5	BQ834924 Po ad 05B
C 18	18.6	84.5	1180	5	BX334080 BX334080
C 19	18.4	83.6	578	8	BH707520 BOHV803TF
C 20	17.8	80.9	324	7	CF933926 T-EST-B16
C 21	17.8	80.9	337	5	BQ488667 91-E8463-
C 22	17.8	80.9	378	8	B32701 HS-1015-B2-
C 23	17.8	80.9	438	6	BY688194 BY688194
C 24	17.8	80.9	440	9	TA168G07P
C 25	17.8	80.9	451	1	AL487440 T. brucei

C 25	17.8	80.9	553	9	TA286C03P
C 26	17.8	80.9	591	8	AQ652813
C 27	17.8	80.9	600	8	AZ215044 Sheared D
C 28	17.8	80.9	649	2	AW318752 un05h01.y
C 29	17.8	80.9	649	5	BQ584470
C 30	17.8	80.9	724	7	CF866553 tric007xb
C 31	17.8	80.9	767	8	BH402703 AG-ND-119
C 32	17.8	80.9	773	7	CF681267 CCAIC82TR
C 33	17.8	80.9	803	6	CB896532 tric007xb
C 34	17.8	80.9	806	7	CF707757 CCAGY25TR
C 35	17.8	80.9	831	6	CB900843 tric024x1
C 36	17.8	80.9	831	7	CF870649 tric024x1
C 37	17.4	79.1	478	2	BE841995 MR4-ST009
C 38	17.4	79.1	490	2	AW581806 MR4-ST009
C 39	17.4	79.1	492	2	AW807650 MR4-ST009
C 40	17.4	79.1	636	8	AQ499367 HS_5199_B
C 41	17.4	79.1	673	5	BP152234 BP152234
C 42	17.4	79.1	973	4	BG709561
C 43	17.2	78.2	212	7	CK817477 hag9009xk
C 44	17.2	78.2	275	2	AW865771 QV3-SN002
C 45	17.2	78.2	322	1	AA319302 EST21987

ALIGNMENTS

RESULT 1
AW386118/c
LOCUS
RC3-PT0003-241199-011-d10 PT0003 Homo sapiens cDNA, mRNA linear EST 04-FEB-2000
DEFINITION
AW386118
ACCESSION
AW386118.1 GI:6890777
VERSION
EST
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 403)
HCGP <http://www.ludwig.org.br/ORESTES>.
AUTHORS
The FAPESP/LICR Human Cancer Genome Project
TITLE
Unpublished (1999)
JOURNAL
Laboratory of Cancer Genetics
COMMENT
Contact: Simpson A.J.G.
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tbl=RC3&tbl2=RC3-PT0003-241199-011-d10&tbl3=1999-11-24&tbl4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 403.
Location/Qualifiers
1..403
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="PT0003"
/note="Organ: pnet; Vector: puc18; Site: 1; Small; Site 2: Small; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 22; DB 2; Length 403;
Best Local Similarity 100.0%; Pred. No. 4.7;

Matches	22; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	1	GATGCTGAAGTCGCTCATTGG	22		
Db	368	GATGCTGAAGTCGCTCATTGG	347		
RESULT 2					
AA905101					
LOCUS	ok05q06.s1 Soares NFL T.GBC.S1	451 bp	mRNA	linear	EST 09-JUN-1998
DEFINITION	IMAGE:1507354 3', mRNA sequence.				
ACCESSION	AA905101				
VERSION	AA905101.1	GI:3040224			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 451)				
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.				
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 853 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 420.				
FEATURES	Location/Qualifiers				
source	1..451				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:1507354"				
	/lab_host="DH10B"				
	/clone_lib="Soares NFL T.GBC.S1"				
	/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."				
ORIGIN					
Query Match	100.0%;	Score 22;	DB 1;	Length 451;	
Best Local Similarity	100.0%;	Pred. No. 4.8;			
Matches	22; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	1	GATGCTGAAGTCGCTCATTGG	22		
Db	411	GATGCTGAAGTCGCTCATTGG	432		
RESULT 3					
AW173368					
LOCUS	xj78f06.x1 Soares NFL T.GBC.S1	493 bp	mRNA	linear	EST 16-NOV-1999
DEFINITION	IMAGE:2663363 3', mRNA sequence.				
ACCESSION	AW173368				
VERSION	AW173368.1	GI:6439316			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	1 (bases 1 to 493)				
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.				
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1553 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 469.				
FEATURES	Location/Qualifiers				
source	1..514				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:2070074"				
ORIGIN					
Query Match	100.0%;	Score 22;	DB 2;	Length 493;	
Best Local Similarity	100.0%;	Pred. No. 4.8;			
Matches	22; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	1	GATGCTGAAGTCGCTCATTGG	22		
Db	467	GATGCTGAAGTCGCTCATTGG	488		
RESULT 4					
AI804454					
LOCUS	tc7le02.x1 Soares NHMPu_S1	514 bp	mRNA	linear	EST 13-DEC-1999
DEFINITION	3', mRNA sequence.				
ACCESSION	AI804454				
VERSION	AI804454.1	GI:5369926			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 514)				
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.				
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1553 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 469.				
FEATURES	Location/Qualifiers				
source	1..514				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:2070074"				

/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
 /lab_host="DH10B"
 /clone_lib="Soares_NhWMPu_S1"
 /notes="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NhWMPu, and fetal heart NBHH19W) were mixed, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

ORIGIN

Query Match 100.0%; Score 22; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTCATGG 22
 |||||
 Db 453 GATGCTGAAGTCGTCCTCATGG 474

RESULT 5

AI082809
 LOCUS
 DEFINITION OX78a02.x1 Soares_NhWMPu_S1 Homo sapiens cDNA clone IMAGE:1662410 3', mRNA sequence.

ACCESSION AI082809
 VERSION AI082809.1 GI:3417785
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 531)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 902 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 451.

FEATURES

Location/Qualifiers
 1..531
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1662410"
 /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
 /lab_host="DH10B"
 /clone_lib="Soares_NhWMPu_S1"
 /notes="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NhWMPu, and fetal heart NBHH19W) were mixed, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

ORIGIN

Query Match 100.0%; Score 22; DB 1; Length 531;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTCATGG 22
 |||||
 Db 453 GATGCTGAAGTCGTCCTCATGG 474

RESULT 6
 AI768516
 LOCUS
 DEFINITION wh22g11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2381540 3', mRNA sequence.

ACCESSION AI768516
 VERSION AI768516.1 GI:5235025
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 554)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
 Insert Length: 766 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 463.

FEATURES
 Location/Qualifiers
 1..554
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2381540"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Kid11"
 /notes="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP Kids was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 100.0%; Score 22; DB 1; Length 554;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCCTCATGG 22
 |||||
 Db 446 GATGCTGAAGTCGTCCTCATGG 467

RESULT 7
 BE466421
 LOCUS
 DEFINITION hz21e08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3208646 3', mRNA sequence.

ACCESSION BE466421
 VERSION BE466421.1 GI:9512293
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 555)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
 info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 453.
 Location/Qualifiers
 1..555
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3208646"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP GC6"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
 from the normalized library NCI-CGAP_GC4 was prepared, and
 ss circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 1257096-1258631, 1469064-1470983, and 1475592-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 100.0%; Score 22; DB 2; Length 555;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCTCATTGG 22
 ||||||||||||||||||
 Db 447 GATGCTGAAGTCGTCTCATTGG 468
 ||||||||||||||||||

RESULT 8
 NC308828/c
 LOCUS NC308828 654 bp mRNA linear EST 16-MAY-2004
 DEFINITION 17000600172033 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION NC308828
 VERSION NC308828.1 GI:47325242
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 654)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
 Lebkowski, J. and Stanton, R.W.
 Transcriptional characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 Contact: Brandenberger R

FEATURES
 source
 1..654
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, DMSO-treated H9 cell
 line"
 /clone_lib="GRN_PREHEP"
 /note="Oligo dT primed, full-length enriched cDNA library
 from DMSO-treated HES cell line H9 (p22) maintained in
 feeder-free conditions"

ORIGIN
 Query Match 100.0%; Score 22; DB 7; Length 654;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCTCATTGG 22
 ||||||||||||||||||
 Db 130 GATGCTGAAGTCGTCTCATTGG 109
 ||||||||||||||||||

RESULT 9
 NC308828/c
 LOCUS NC308828 687 bp mRNA linear EST 17-JUN-2002
 DEFINITION UI-H-DTI-awb-a-01-0-UI.s1 NCI-CGAP_DTI Homo sapiens cDNA clone
 IMAGE:5886984 3', mRNA sequence.
 ACCESSION NC308828
 VERSION NC308828.1 GI:19751343
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 687)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Seq primer: M13 FORWARD
 POLYA-Yes.

FEATURES
 source
 1..687
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5886984"
 /tissue_type="Metastatic Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP DTI"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP DTI is a normalized cDNA library containing the
 following tissue(s): Metastatic Chondrosarcoma in Lung.
 The library was constructed according to Bonaldo, Lennon
 and Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer

Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 654 Std Error: 0.00.
 Location/Qualifiers
 1..654
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, DMSO-treated H9 cell
 line"
 /clone_lib="GRN_PREHEP"
 /note="Oligo dT primed, full-length enriched cDNA library
 from DMSO-treated HES cell line H9 (p22) maintained in
 feeder-free conditions"

ORIGIN
 Query Match 100.0%; Score 22; DB 7; Length 654;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCTCATTGG 22
 ||||||||||||||||||
 Db 130 GATGCTGAAGTCGTCTCATTGG 109
 ||||||||||||||||||

RESULT 9
 NC308828/c
 LOCUS NC308828 687 bp mRNA linear EST 17-JUN-2002
 DEFINITION UI-H-DTI-awb-a-01-0-UI.s1 NCI-CGAP_DTI Homo sapiens cDNA clone
 IMAGE:5886984 3', mRNA sequence.
 ACCESSION NC308828
 VERSION NC308828.1 GI:19751343
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 687)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Seq primer: M13 FORWARD
 POLYA-Yes.

FEATURES
 source
 1..687
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5886984"
 /tissue_type="Metastatic Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP DTI"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP DTI is a normalized cDNA library containing the
 following tissue(s): Metastatic Chondrosarcoma in Lung.
 The library was constructed according to Bonaldo, Lennon
 and Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer

containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7733-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AACTGTTCGG.

TAG_TISSUE=lung metastatic chondrosarcoma
TAG_LIB=UI-H-DT1
TAG_SEQ=AACTGTTCGG"

ORIGIN

Query Match 100.0%; Score 22; DB 5; Length 687;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTGG 22
|||||
Db 467 GATGCTGAAGTCGTCCTCATTTGG 488

RESULT 10

BQ002692 782 bp mRNA linear EST 26-MAR-2002
LOCUS UI-H-E11-ayu-1-16-0-UI.s1 NCI_CGAP_E11 Homo sapiens cDNA clone
IMAGE:5843871 3', mRNA sequence.

ACCESSION BQ002692
VERSION BQ002692
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 782)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES

source

1..782 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5843871"
/tissue_type="Chondrosarcoma"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_E11"

/note="Organ: Left Pelvis; Vector: p7733-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_E11 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-805, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7733-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AACTGTTCAC.
TAG_TISSUE=chondrosarcoma

TAG_LIB=UI-H-E11
TAG_SEQ=AACTGTTCAC"

ORIGIN

Query Match 100.0%; Score 22; DB 5; Length 782;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTGG 22
|||||
Db 463 GATGCTGAAGTCGTCCTCATTTGG 484

RESULT 11

BG283778 895 bp mRNA linear EST 21-FEB-2001
LOCUS BG283778/c 602408077F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4520179 5',
mRNA sequence.

ACCESSION BG283778
VERSION BG283778
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 895)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10417 row: j column: 20
High quality sequence stop: 610.

FEATURES

source

1..895 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4520179"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_91"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 22; DB 4; Length 895;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGAAGTCGTCCTCATTTGG 22
|||||
Db 296 GATGCTGAAGTCGTCCTCATTTGG 275

RESULT 12

BG786617 901 bp mRNA linear EST 20-OCT-2000
LOCUS BG786617/c 601478845F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881579 5',
mRNA sequence.

ACCESSION BE786617
VERSION BE786617.1 GI:10207815
KEYWORDS EST.

```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 901)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           Tissue Procurement: DCTD/DRP/Gazdar
           cDNA Library Preparation: Life Technologies, Inc.
           DNA Sequencing by: Incyte Genomics, Inc.
           Cloned through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLM9650 row: j column: 12
           High quality sequence start: 10
           High quality sequence stop: 596.
           Location/Qualifiers
             1..901
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:3881579"
               /tissue_type="large cell carcinoma"
               /lab_host="DH10B (phage-resistant)"
               /clone_lib="NIH MGC 68"
               /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
               Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
               Average insert size 1.8 Kb. Library constructed by Life
               Technologies."
ORIGIN
  Query Match      100.0%; Score 22; DB 2; Length 901;
  Best Local Similarity 100.0%; Pred. No. 5.1;
  Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCTCATGG 22
    |||||
DB 167 GATGCTGAAGTCGTCTCATGG 146

RESULT 13
BG546951/c
LOCUS      BG546951
DEFINITION BG546951 901 bp mRNA linear EST 04-APR-2001
           mRNA sequence.
ACCESSION  BG546951
VERSION    BG546951.1 GI:13545616
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  1 (bases 1 to 901)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           Tissue Procurement: CLONTECH Laboratories, Inc.
           cDNA Library Preparation: CLONTECH Laboratories, Inc.
           DNA Sequencing by: Incyte Genomics, Inc.
           Cloned through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLM1538 row: e column: 12
           High quality sequence stop: 751.
           Location/Qualifiers
             1..901
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:4702067"
               /tissue_type="embryonal carcinoma, cell line"
               /lab_host="DH10B (phage-resistant)"
               /clone_lib="NIH MGC 92"
               /note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
               Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
               Average insert size 2.5 kb. Library enriched for
               full-length clones and constructed by Life Technologies.
               Note: this is a NIH_MGC Library."
FEATURES
  source
    Query Match      100.0%; Score 22; DB 4; Length 943;
    Best Local Similarity 100.0%; Pred. No. 5.1;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4702067"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 77"
/note="Organ: lung; Vector: pCMV-LIB (Clontech); Site 1:
SfiI (ggccctcgcc); Site 2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
ORIGIN
  Query Match      100.0%; Score 22; DB 4; Length 901;
  Best Local Similarity 100.0%; Pred. No. 5.1;
  Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCTGAAGTCGTCTCATGG 22
    |||||
DB 226 GATGCTGAAGTCGTCTCATGG 205

RESULT 14
BG388221/c
LOCUS      BG388221
DEFINITION BG388221 943 bp mRNA linear EST 12-MAR-2001
           mRNA sequence.
ACCESSION  BG388221
VERSION    BG388221.1 GI:13281667
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  1 (bases 1 to 943)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Cloned through the I.M.A.G.E. Consortium/LLNL at:
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLM10421 row: 1 column: 04
           High quality sequence stop: 766.
           Location/Qualifiers
             1..943
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:4521747"
               /tissue_type="embryonal carcinoma, cell line"
               /lab_host="DH10B (phage-resistant)"
               /clone_lib="NIH MGC 92"
               /note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
               Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
               Average insert size 2.5 kb. Library enriched for
               full-length clones and constructed by Life Technologies.
               Note: this is a NIH_MGC Library."
FEATURES
  source
    Query Match      100.0%; Score 22; DB 4; Length 943;
    Best Local Similarity 100.0%; Pred. No. 5.1;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


Qy 1 GATCGTGAAGTCGTCTCATTGG 22
|||||
Db 394 GATCGTGAAGTCGTCTCATTGG 373

RESULT 15
HSM801459/c
LOCUS HSM801459 4308 bp mRNA linear HTC 22-SEP-2004
DEFINITION Homo sapiens mRNA; cDNA DKFZp434G0715 (from clone DKFZp434G0715).
ACCESSION AL133605
VERSION AL133605.1 GI:6599213
KEYWORDS HTC.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4308)
Bloembergen, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B., Amid, C.,
Oanger, A., Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY

REFERENCE
AUTHORS Clon from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
CONSRTM This clone (DKFZp434G0715) is available at the RZPD Deutsches
Reesourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
TITLE Please contact RZPD for ordering:
JOURNAL http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp434G0715
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES
source
1..4308
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp434G0715"
/tissue_type="testis"
/clone_lib="434 (synonym: htes3). Vector pSport1; host
DH10B; sites NotI + SalI"
/dev_stage="adult"
/notes="pallino 2, N-terminus truncated"

gene
1..4308
CDS
1..150
/gene="DKFZp434G0715"
/codon_start=1
/product="hypothetical protein"
/protein_id="CAH56388.1"
/db_xref="GI:52545575"
/translation="VCSEKSAKYWSQIPLPHGTHAFHAACPFCATQLVGEQNCIKLIP
QGPID"

ORIGIN
Query Match 100.0%; Score 22; DB 3; Length 4308;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATCGTGAAGTCGTCTCATTGG 22
|||||
Db 3846 GATCGTGAAGTCGTCTCATTGG 3825

Search completed: July 20, 2005, 18:56:21
Job time : 1582.48 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 15:43:06 ; Search time 1716.52 Seconds
(without alignments)
532.206 Million cell updates/sec

Title: US-10-041-030-8

Perfect score: 24

Sequence: 1 ccagtagtttagccttggctt 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsel:*
9: gb_gsel2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	24	100.0	214	AW272021	AW272021 xr45b04.x
C 2	24	100.0	295	BI038270	BI038270 RC5-WT026
C 3	24	100.0	531	AI082809	AI082809 ox78a02.x
C 4	24	100.0	554	AI768516	AI768516 wh22g11.x
C 5	24	100.0	654	CN308828	CN308828 170006001
C 6	24	100.0	687	BQ016066	BQ016066 UI-H-DT1-
C 7	24	100.0	782	BQ002692	BQ002692 UI-H-E11-
C 8	24	100.0	895	EG283778	EG283778 602408077
C 9	24	100.0	901	EG546951	EG546951 602573943
C 10	24	100.0	943	EG388221	EG388221 602413214
C 11	24	100.0	4308	HSW801459	HSW801459 Homo sapi
C 12	23	95.8	555	BE466421	BE466421 h221e08.x
C 13	22.4	93.3	274	BQ091930	BQ091930 UNM17E05
C 14	22.4	93.3	403	AW386118	AW386118 RC3-PT000
C 15	20.8	86.7	171	CB117270	CB117270 K-EST0162
C 16	19.2	80.0	101	N99024	N99024 za67f06.r1
C 17	19.2	80.0	173	BI001452	BI001452 MR3-HN012
C 18	19.2	80.0	228	BI001750	BI001750 MR3-HN014
C 19	19.2	80.0	243	BI001761	BI001761 MR3-HN014
C 20	19.2	80.0	265	BQ359661	BQ359661 MR3-HN014
C 21	19.2	80.0	332	AA617629	AA617629 np34g08.s
C 22	19.2	80.0	462	AI822085	AI822085 za92h12.y
C 23	19.2	80.0	492	BM996453	BM996453 UI-H-DT0-
C 24	19.2	80.0	634	BM970838	BM970838 UI-CF-EC1

C	25	19.2	80.0	635	2	BB578089	BB578089
	26	19.2	80.0	725	6	CA502940	CA502940 UI-CF-PNO
	27	19.2	80.0	777	5	BX443706	BX443706 BX443706
	28	19.2	80.0	919	5	BX372042	BX372042 BX372042
C	29	19.2	80.0	1692	3	CR600885	CR600885 full-leng
C	30	19.2	80.0	2280	3	CR604190	CR604190 full-leng
C	31	18.8	78.3	198	5	BQ095095	BQ095095 Kk12h10.y
C	32	18.8	78.3	437	5	BY001426	BY001426 BY001426
C	33	18.8	78.3	591	9	CR189890	CR189890 Reverse s
C	34	18.8	78.3	644	9	CE192848	CE192848 t1gr-988-
C	35	18.8	78.3	645	2	BE911617	BE911617 601663094
C	36	18.8	78.3	1180	5	BX334080	BX334080 BX334080
C	37	18.4	76.7	539	7	CO585167	CO585167 DG2-11111
C	38	18.4	76.7	562	7	CO586470	CO586470 DG2-131a6
C	39	18.4	76.7	576	7	CO716806	CO716806 DG14-30k2
C	40	18.4	76.7	579	7	CO699795	CO699795 DG32-166b
C	41	18.4	76.7	600	7	CO696308	CO696308 DG11-96n1
C	42	18.4	76.7	628	7	CO591703	CO591703 DG2-53f18
C	43	18.4	76.7	631	7	CO588078	CO588078 DG2-19d14
C	44	18.4	76.7	637	7	CO588492	CO588492 DG2-2115
C	45	18.4	76.7	640	7	CO693480	CO693480 DG11-63a1

ALIGNMENTS

RESULT 1
AW272021/c
LOCUS
DEFINITION
xr45b04.x1 NCI CGAP_Ov26 Homo sapiens cDNA clone IMAGE:2763055 3',
mRNA;sequence.
ACCESSION
AW272021
VERSION
AW272021.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 214)
AUTHORS
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLES
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Cloned by: Washington University Genome Sequencing Center
Cloned Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.

FEATURES

1..214
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2763055"
/sex="female"
/tissue_type="papillary serous carcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Ov26"
/note="Organ: ovary; Vector: pAMP1; mRNA made from
papillary serous ovarian carcinoma, cDNA made by oligo-dT
priming. Directionally cloned. Size-selected on agarose
gel, average insert size 500 bp. Primary library,
non-amplified."

ORIGIN

Query Match 100.0%; Score 24; DB 2; Length 214;

Best Local Similarity 100.0%; Pred. No. 1.5; Mismatches 0; Gaps 0; Indels 0; Mismatches 0; Gaps 0; Indels 0;

QY 1 CCAGTAGTTAGCCTTTGGCTT 24
Db 57 CCAGTAGTTAGCCTTTGGCTT 34

RESULT 2
BI038270/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

295 bp mRNA linear EST 14-JUN-2001
RC5-NT0266-180101-011-B12 NT0266 Homo sapiens cDNA, mRNA sequence.
BI038270
BI038270.1 GI:14444896
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-NT0266-180101-011-B12&t3=2001-01-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 28
High quality sequence stop: 294.
Location/Qualifiers
1. .295
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0266"
/notes="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORFEST PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Query Match 100.0%; Score 24; DB 4; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.6; Mismatches 0; Gaps 0; Indels 0; Mismatches 0; Gaps 0; Indels 0;

QY 1 CCAGTAGTTAGCCTTTGGCTT 24
Db 60 CCAGTAGTTAGCCTTTGGCTT 37

RESULT 3
AI082809/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

554 bp mRNA linear EST 20-DEC-1999
wh22g11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2381540 3', mRNA sequence.
AI768516
AI768516.1 GI:5235025
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

531 bp mRNA linear EST 24-SEP-1998
ox78a02.x1 Soares_NhMpu_S1 Homo sapiens cDNA clone IMAGE:1662410 3', mRNA sequence.
AI082809
AI082809.1 GI:3417785
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 902 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 451.
Location/Qualifiers
1. .531
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:1662410"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_hosts="DH10B"
/clone_lib="Soares_NhMpu_S1"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NBHPU, and fetal heart NBH19W) were mixed, and ss circles were used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

Query Match 100.0%; Score 24; DB 1; Length 531;
Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Gaps 0; Indels 0; Mismatches 0; Gaps 0; Indels 0;

QY 1 CCAGTAGTTAGCCTTTGGCTT 24
Db 526 CCAGTAGTTAGCCTTTGGCTT 503

RESULT 4
AI768516/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

554 bp mRNA linear EST 20-DEC-1999
wh22g11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2381540 3', mRNA sequence.
AI768516
AI768516.1 GI:5235025
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 766 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 463.
 Location/Qualifiers
 1. .554
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2381540"
 /lab_hosts="DH10B"
 /clone_lib="NCI CGAP Kid11"
 /notes="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP Kid3 was prepared, and 88 circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDa 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 24; DB 1; Length 554;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTAGCCTTTGGCTT 24

|||||
 Db 519 CCAGTAGTTAGCCTTTGGCTT 496

RESULT 5

CN308828 1700600172033 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence. EST 16-MAY-2004
 LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Brandenberger R
 Regenerative Medicine
 Genon Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@genon.com
 Insert Length: 654 Std Error: 0.00.
 Location/Qualifiers
 1. .654
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, DMSO-treated H9 cell line"

FEATURES

source

Query Match 100.0%; Score 24; DB 5; Length 687;
 Best Local Similarity 100.0%; Pred. No. 1.8;

ORIGIN

Query Match 100.0%; Score 24; DB 7; Length 654;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCAGTAGTTAGCCTTTGGCTT 24
 |||||
 Db 57 CCAGTAGTTAGCCTTTGGCTT 80

RESULT 6

BQ016066/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ016066 687 bp mRNA linear EST 17-JUN-2002
 UI-H-DTI-awb-a-01-0-UI.81 NCI CGAP_DTI Homo sapiens cDNA clone
 IMAGE:5886984 3', mRNA sequence.
 BQ016066
 BQ016066.1 GI:19751343
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 687)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

Location/Qualifiers
 1. .687
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5886984"
 /tissue_type="Metastatic Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP DT1"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP DT1 is a normalized cDNA library containing the following tissue(s): Metastatic Chondrosarcoma in Lung.
 The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AACTGTTCCG.
 TAG TISSUE=lung metastatic chondrosarcoma
 TAG_LiB=UI-H-DTI
 TAG_SEQ=AACTGTTCCG"

ORIGIN

Query Match 100.0%; Score 24; DB 5; Length 687;
 Best Local Similarity 100.0%; Pred. No. 1.8;

/clone_lib="GRN PREHEP"
 /note="oligo dT primed, full-length enriched cDNA library from DMSO-treated HES cell line H9 (p22) maintained in feeder-free conditions"

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAGTAGTTAGCCTTTGGCTT 24
Db 540 CCAGTAGTTAGCCTTTGGCTT 517

RESULT 7
BQ002692/c
LOCUS
DEFINITION
UI-H-E11-ayv-l-16-0-UI.s1 NCI CGAP_E11 Homo sapiens CDNA clone
IMAGE:5843871 3', mRNA sequence.
ACCESSION
VERSION
BQ002692
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 782)
REFERENCE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1..782
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5843871"
/issue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_E11"
/notes="Organ: Left Pelvis; Vector: pTT3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP_E11 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pTT3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
ACACTTGCAC.
TAG TISSUE=chondrosarcoma
TAG LIB=UI-H-E11
TAG_SEQ=ACACTTGCAC"

ORIGIN
Query Match 100.0%; Score 24; DB 5; Length 782;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAGTAGTTAGCCTTTGGCTT 24
Db 536 CCAGTAGTTAGCCTTTGGCTT 513
RESULT 8

BG283778
LOCUS
DEFINITION
602408077F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4520179 5',
mRNA sequence.
ACCESSION
VERSION
BG283778
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 895)
REFERENCE
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10417 row: j column: 20
High quality sequence stop: 610.

FEATURES
source
1..895
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4520179"
/issue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_91"
/note="Organ: prostate; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 100.0%; Score 24; DB 4; Length 895;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAGTAGTTAGCCTTTGGCTT 24
Db 223 CCAGTAGTTAGCCTTTGGCTT 246

RESULT 9
BG546951
LOCUS
DEFINITION
602573943F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4702067 5',
mRNA sequence.
ACCESSION
VERSION
BG546951
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 901)
REFERENCE
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

ORIGIN
Query Match 100.0%; Score 24; DB 5; Length 782;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAGTAGTTAGCCTTTGGCTT 24
Db 536 CCAGTAGTTAGCCTTTGGCTT 513
RESULT 8

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: L1CM1538 row: e column: 12
High quality sequence stop: 751.
Location/Qualifiers

FEATURES
source

```
1. .901
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:470267"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC 77"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 Kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
```

ORIGIN

Query Match 100.0%; Score 24; DB 4; Length 901;
Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTTTCAGCTTTGTGGCTT 24
|||||
DB 153 CCAGTAGTTTTCAGCTTTGTGGCTT 176

RESULT 10

BG388221
LOCUS 602413214F1 NIH_MGC_92 943 bp mRNA linear EST 12-MAR-2001
DEFINITION mRNA sequence.

ACCESSION BG388221
VERSION BG388221.1 GI:13281667
KEYWORDS EST.

SOURCE

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 943)
NIH-MGC <http://imgc.nci.nih.gov/>.

REFERENCE

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM10421 row: 1 column: 04

High quality sequence stop: 766.
Location/Qualifiers

FEATURES

source

```
1. .943
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4521747"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 92"
/notes="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for
```

full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 24; DB 4; Length 943;
Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTTTCAGCTTTGTGGCTT 24
|||||
DB 321 CCAGTAGTTTTCAGCTTTGTGGCTT 344

RESULT 11

HS801459
LOCUS HS801459 4308 bp mRNA linear HTC 22-SEP-2004
DEFINITION Homo sapiens mRNA; cDNA DKFZp434G0715 (from clone DKFZp434G0715).
ACCESSION AL133605
VERSION AL133605.1 GI:6599213

KEYWORDS

HTC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4308)
Bloeker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B., Amid, C.,
Oanger, A., Fodor, G., Han, M. and Wiemann, S.

CONSRMT

Direct Submission

TITLE

Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764

JOURNAL

Neuberberg, GERMANY

COMMENT

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GSF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.

This clone (DKFZp434G0715) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.

Please contact RZPD for ordering:
<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp434G0715>

Further information about the clone and the sequencing project is
available at <http://mips.gsf.de/projects/cdna/>.

Location/Qualifiers

FEATURES

source

```
1. .4308
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp434G0715"
/tissue_type="testis"
/clone_lib="434 (synonym: htes3). Vector pSport1; host  
DH10B; sites NotI + SalI"
```

gene

1. .4308

/gene="DKFZp434G0715"

CDS

1. .150

/gene="DKFZp434G0715"

/codon_start=1

/product="hypothetical protein"

/protein_id="CAH56388.1"

/db_xref="GI:52545575"

/translation="VCSEKSAKYWSQIPLPHGTHAFHAACPFCATQLVGEQNCIKLIF
QGPID"

ORIGIN

Query Match 100.0%; Score 24; DB 3; Length 4308;
Best Local Similarity 100.0%; Pred. No. 2.4; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGTAGTTTTCAGCTTTGTGGCTT 24
|||||
DB 3773 CCAGTAGTTTTCAGCTTTGTGGCTT 3796

RESULT 12
 BE466421/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 HOMO sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 555)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 453.
 Location/Qualifiers
 1..555
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3208646"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP GC6"
 /note="Vector: p7T3D-pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
 from the normalized library NCI CGAP GC4 was prepared, and
 as circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (cloneids
 1257096-1258631, 1469064-1470983, and 1475592-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaldo."

FEATURES source

Query Match 95.8%; Score 23; DB 2; Length 555;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CAGTAGTTTACGCTTTGTGGCTT 24
 |||||
 Db 519 CAGTAGTTTACGCTTTGTGGCTT 497

RESULT 13
 BQ091930/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Canis familiaris (dog)
 Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 274)

AUTHORS JOURNAL COMMENT

Roberts, M.C., Hendrickson, J.A., Hoffmann, D.E., Flickinger, G.H.,
 Rutherford, M.S., and Mickelson, J.R.
 University of Minnesota Canine Brain EST Project
 Unpublished (2001)
 Contact: Mickelson, J.R.
 Veterinary Pathobiology
 University of Minnesota
 1988 Fitch Avenue, University of Minnesota, St. Paul, MN 55108, USA
 Tel: 612 624 1246
 Fax: 612 625 0204
 Email: mick001@umn.edu
 Seq primer: M13 Reverse.

FEATURES source

1..274
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /db_xref="taxon:9615"
 /sex="Male"
 /clone_lib="Canine Brain cDNA Library"
 /note="Organ: Brain; Vector: pSPORT1 (Gibco BRL); Site_1:
 NotI; Site_2: SalI; Tissue was taken from the frontal,
 occipital, temporal and parietal lobes, olfactory bulb,
 hippocampus, cerebellum, thalamus, hypothalamus,
 midbrain, pons, and medulla."

ORIGIN

Query Match 93.3%; Score 22.4; DB 5; Length 274;
 Best Local Similarity 95.8%; Pred. No. 8.8;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCAGTAGTTTACGCTTTGTGGCTT 24
 |||||
 Db 189 CCAGTAGTTTACGCTTTGTGGCTT 166

RESULT 14 AW386118

LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 403)
 HCGP <http://www.ludwig.org.br/ORESTES>.
 The FAPESP/LICR Human Cancer Genome Project
 Unpublished (1999)
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-PT0003-241199-011-d10&t3=1999-11-24&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 403.
 Location/Qualifiers
 1..403
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="PT0003"
 /note="Organ: pnet; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived

FEATURES source

1..403
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="PT0003"
 /note="Organ: pnet; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived

This Page Blank (uspto)